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DEVELOPMENT OF A TOXIN KNOWLEDGE SYSTEM

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Final Summary Report

Harold L. Trammel

November 12, 1990

for the Period April 6, 1987 through December 1, 1989

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<p>The development of a Toxin Knowledge System (TKS) was begun in an attempt to meet the needs for readily accessible toxin knowledge. This system was designed to extract facts from published literature using structured abstracting techniques, store these facts in a standard knowledge structure, control the terminology entered through the use of a standard nomenclature system, and subsequently generate standard monographs on individual toxins. The system uses a relational database management system and associated programming language on a minicomputer. Standard nomenclature systems were created for clinical findings, journal abbreviations, study terminology, and book information. The development of a chemical vocabulary was unsuccessful. The current TKS version is of primary value with papers describing in vivo toxicologic studies. The TKS application facilitates the extraction of needed information from both journals and books through a sophisticated user interface. The user enters citation data and is then prompted for information about each study design (up to 99 per paper), each subject group (up to 99 per design) and exposure regimen (up to 99 per design) within each design, and how these factors interact to produce clinical effects. All reported clinical findings can be entered using the controlled vocabulary. Rudimentary monograph generation capabilities were initiated but need further development. So that USAMRIID personnel can use and further develop the TKS application, the TKS was ported to the MS-DOS platform.</p>					
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Summary

The published information about low molecular weight toxins grows steadily, yet there are few tools to manage this information. The information tools currently used are citation indexes or abstract services. These tools do not integrate facts into an existing knowledge base but merely provide citations or narrative abstracts. To meet the toxin knowledge needs and overcome the limitations of current information systems, a Toxin Knowledge System was created.

After studying the knowledge acquisition techniques used by individuals in different biomedical disciplines, we set out to automate the knowledge acquisition process and compile information into usable, continuously updated knowledge. The Toxin Knowledge System was built using Informix® relational database management system on a Sequent® minicomputer. The user interface application was developed using Informix-4GL® programming language and makes extensive use of windows, ring-menus, and pop-up choices on screen. The system was based on four concepts: a standard knowledge structure, standard nomenclature systems, a structured abstracting process, and computer-generated structured monographs.

The standard knowledge structure into four major parts: citation data, study design, results, and keywords-notes. Multiple database tables were created for each part. Because the interactions between these various tables were so complex, the user interface application had to be designed to manage these interactions with little user involvement.

To ensure that the information entered was consistent, standard nomenclature systems were created for clinical terminology (based on SNOMED/SNOVET), study information (internally developed), journal abbreviations (based on NLM List of Journals Indexed), and book information (internally developed). Attempts to create an efficient chemical vocabulary based on the Registry of Toxic Effects of Chemical Substances were unsuccessful. The user application contained mechanisms to add terms, modify, or delete terms from the various vocabularies.

Control of the structured abstracting process was built into the user application. Currently this process is primarily effective in *in vivo* toxicology studies although other study designs can be included. The application leads the abstractor from the citation data entry through the study materials and methods and on to the clinical effects reported in each subject group exposed to a given toxicant. The system is capable of abstracting papers with up to 99 different study designs, each containing up to 99 subject groups and 99 exposure regimens. For each design-subject group-exposure regimen, an unlimited number of clinical findings can be entered.

The number of computer-generated monographs developed was limited due to personnel shortages. We were able to develop three different monographs to a preliminary stage. The user application uses data entered by the abstractor to create paragraphs describing each clinical finding and the circumstances that created it.

By end of the contract, the Toxin Knowledge System had begun to show the promise that was proposed initially. Unfortunately it was not developed to full operational status due to programming personnel difficulties. The system was ported to the MS-DOS computer platform for further use and development.

Foreword

Citations of commercial organizations or trade names in this report do not constitute an official Department of the Army endorsement or approval of the products or services of these organizations.

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Toxin Knowledge System Final Report

1 Statement of Problem

The production and use of toxins against military and civilian populations remains a significant concern. To counteract an enemy attacking with a toxin, military and civil defense personnel need the knowledge to detect the toxin, diagnose the effects caused, and implement appropriate treatment. While the amount of information on toxins continues to grow, there is no system to collect, compile, and update this information into knowledge. Scientific knowledge can be defined as the sum total of what is known about a topic or as a body of systemized facts, information, principles, and experiences relating to a singular topic. Gaining this knowledge is a difficult and time consuming process. Updating this knowledge is even more difficult.

To complicate the problem, the toxin knowledge needs vary with the user. Researchers studying toxins need detailed, up-to-date information from the literature and other research groups. Others, such as military and civil defense health professionals, need extensive information on the detection, diagnosis, and treatment of toxin related problems. Military personnel at risk of exposure to toxins need immediately available references appropriate for the user's training.

Regardless of the toxin information needs, the factual basis for this knowledge is derived from the same literature sources. It would benefit the different interested groups if a single source of collected toxin information could meet each group's needs. This source of toxin information or knowledge should contain detailed, comprehensive information but be able to provide each group with the specific facts and details appropriate for the needs of the group.

To date, the most common means of keeping up with scientific information merely provides access to current literature through citation indexes and abstracting systems. Citation indexes are limited to providing users with journal article citations from which the original article can be obtained. Some form of keyword-based search strategy must be used to find the desired literature citations. A user with a journal citation will still have to find the actual article in order to obtain the facts necessary to add to his/her knowledge. Citation indexes are likely the most important ways to access the published literature and is the foundation of most other information systems. Unfortunately citation indexes are simply pointers to the facts and not the facts themselves. Abstracting systems build on the citation index foundation and add narrative abstracts of the paper. The primary purpose for the abstracts is to improve the efficiency of selecting journal articles for further review. A secondary purpose is to provide facts which increase knowledge on the topic. The amount of scientific information contained in these abstracts is limited. Usually the user will need to obtain and review the original paper to gain the knowledge s/he needs.

2 The Knowledge Acquisition Process

A scientist acquiring knowledge from the literature takes advantage of certain standard structures and terminologies. In using citation indexes and/or abstracting systems, s/he selects papers based on a standard keyword vocabulary. S/he uses the standard citation structure to identify the papers to be reviewed. This structure includes both the format of the citation and the standard abbreviations used.

After obtaining the desired papers, the scientist begins to read the papers and thereby uses the format used to write scientific papers. Each discipline has its own particular format and most papers from a given discipline are prepared according to that format. The standard format facilitates the scientist's identification of the critical components of the study design and the associated results and conclusions.

Frequently the scientist will sort the papers by the study design used. S/he may group the papers by case reports and animal studies. From this sorting, the scientist may further group the papers by the materials and methods. For example, s/he might group papers by dosage regimens to consider them from a dose-response perspective. The reader may have to sort the papers several times in various ways in order to obtain an understanding of the study and its results.

When the authors of a scientific paper wrote the paper, their goal was to communicate how their work was performed and what their results were. They used "standard" terms in order to assure that the reader would understand what they did and saw. This is especially true with clinical findings seen as result of the study. If the scientist reading the paper is unfamiliar with a particular term, s/he must either "translate" it into a term s/he already knows or add this term to his/her vocabulary. Subsequently the reviewer will consider the author's discussion of results. Frequently the discussion in current papers will provide both a reference to and an evaluation of older papers.

The data from the individual papers must be integrated into a cohesive form by the scientist. The result data from the various papers are considered by the reviewer as groups of results, along with the study design, materials and methods used, and conclusions drawn from the results. The form that the scientist's summary may take is quite varied. The end result can be a printed monograph on the topic, or may be kept only in the mind of the scientist.

Unfortunately, textual materials, such as reference books, monographs, and text books, are frequently neglected in this process. Too often, the scientist seeks his/her answers only in current literature with limited success, and yet part or all of the answers may have been published several years earlier and summarized in textual materials. Many times these important sources of information yield a deeper understanding, especially with regard to the historical development of an idea or procedure. This information should be included along with current journal articles to provide a more comprehensive understanding.

3 Approach to Problem

We studied the knowledge acquisition techniques used by individuals in different biomedical disciplines. This analysis revealed common methods and procedures as well as commonly accepted needs for how the knowledge should be made available. We believed the knowledge acquisition process could be automated to a significant degree and that we could develop a systemized method to extract needed data about toxins and compile that data into usable, continuously updated knowledge. This method would be based on a standard knowledge structure, use standard nomenclature systems and a structured abstracting process, and create structured monographs. To permit the user to interact with this knowledge system, a computer program would be needed.

We used a relational database management system and a minicomputer to manage the standard knowledge structure. As an abstractor read a journal or textual information

source, s/he would interact with the database via a computer program which would present questions and prompts to be completed by the abstractor using data from the papers. The data would be stored in various database tables. The underlying processes which maintain the database, such as links between tables, would be hidden from the user.

4 Results

4.1 Standard Knowledge Structure

The standard knowledge structure for the Toxin Knowledge System is primarily a complex relational database created with Informix-SQL® relational database management software on a Sequent® minicomputer. To provide access to this structure we used Informix-4GL®, a true fourth-generation computer language for Informix-based databases which permitted us to utilize the strengths of Informix-SQL® for the general database management process and have essentially full control over the user interface design.

We divided the knowledge structure into four major parts: citation data, study design, results, and keywords-notes. Database tables were created for each part. Because all data entered would be derived from a scientific publication, the citation database table was considered the primary entity. The primary foreign key used to relate data from all tables was a citation number derived from the journal, volume, page number, and year. In addition each record in all data tables were given a unique serial number. Within the paper content data tables, these serial numbers were used as additional keys between the tables.

Appendix A shows a graphical representation of the database design and Appendix B presents the details of the database design as text. The tables that were created for nomenclature data are also presented in Appendix A and B.

4.2 Standard Nomenclature

The standard nomenclature was primarily implemented in the form of "lookup" tables within the TKS database structure. Smaller portions of the standard nomenclature were integrated within the application as translation functions and on-screen choices. Considerable programming effort was needed to incorporate the standard nomenclature tables in an efficient manner.

4.2.1 Journal Vocabulary Table

In order to assure that journal abbreviations were consistent and to reduce the number of keystrokes needed to enter citation data, a database table to hold the journal reference data was created. This table, *journalst*, serves as a journal name controlled vocabulary. Each journal title was assigned a code number consisting of the letter "J" followed by a sequentially assigned accession number. This jcode is used as a link to the citation table. The journal title and abbreviation used was usually consistent with the National Library of Medicine (NLM) List of Journals Indexed. Abbreviations and titles for journals not found in this list were taken from the journals themselves.

To make the vocabulary as unobtrusive as possible, the application permitted journal names and abbreviations to be added to the vocabulary as needed, even while the user was putting journal citation data into the computer. A program module to manage the journal vocabulary data was developed. This program automatically assigns the sequential accession number and generates the code value for any new journal added to the vocabulary.

The user can search for any item in the journal vocabulary and update or delete it as is needed.

4.2.2 Book Vocabulary Table

Similarly, a table to hold book reference data was created and an Informix-4GL® program module prepared to manage this table. Booklst contains all the elements necessary to identify the specific book. Each book is assigned a code number consisting of the letter "B" and a sequentially assigned accession number. This code is used to link the book data to the citation table. Book data is entered as needed and can be added while the user is entering book citation data.

4.2.3 Study Information Terminology

As the structured abstract process was being developed, the data used in pop-up options on entry and update screens for study design, subject group, and exposure regimen became a controlled vocabulary. This was further reinforced when the monograph generation efforts began. The user had to choose the correct term at the data entry time in order to get the correct term in the monograph.

A separate aspect of study information terms was encountered in devising a listing of keywords to be used in the Keywords table. This listing is presented in Appendix C.

4.2.4 Clinical Finding Controlled Vocabulary

We hoped use an existing vocabulary for clinical findings and considered three such vocabularies: the National Library of Medicine Medical Subject Headings (MeSH), the World Health Organization International Classification of Diseases (ICD), and the American College of Pathology SNOMED and associated American Veterinary Medical Association SNOVET. The MeSH and the ICD were considered to have strength in disease terminology but did not have the specific pathology information necessary to describe clinical findings in published papers. Both were easily understood and could be used with limited modification for human data. Neither system was considered adequate for describing clinical findings in animals, a necessity when describing the results of animal studies. The ICD had no specific veterinary terms and the MeSH had a very limited set of such terms.

SNOMED was human-oriented and inadequate for veterinary or animal-research descriptions; however, SNOVET had been designed to be a animal-oriented superset of SNOMED and therefore included terms not in SNOMED. The SNOMED/SNOVET combination was determined to be the most appropriate base for a clinical finding vocabulary as it provided a broad set of specific pathologic terms applicable to both human and animal settings. Although the structure of the SNOMED and SNOVET computer tapes were dissimilar, we merged the terms into a species independent vocabulary.

The primarily obstacle we had to overcome in using the SNOMED/SNOVET coding system was its multiple axis arrangement. A user would have to enter 3 to 6 code numbers to characterize one clinical finding. We concluded that this multi-axis approach was too awkward and complex to use. We attempted to overcome the multi-axis difficulties by integrating the various SNOMED/SNOVET tables into a single, more cohesive system. This proved to be inefficient and awkward as well.

We eventually devised a two-tiered controlled vocabulary arrangement. The first tier consisted of a database table containing a frequently used subset of clinical findings ex-

tracted from the SNOMED/SNOVET tables. The first tier would also have a synonym table that would provide a lookup method for the first tier controlled vocabulary. If the desired clinical finding were not in the small controlled vocabulary or the synonym list, the user would be able to access the full SNOMED/SNOVET listing in the second tier. In this way, the usual data entry process would work at acceptable speed and only occasionally would the slower, full SNOMED/SNOVET access be needed.

This internally designed system divided the vocabulary into Site and Effect which was further divided into three broad areas: laboratory analysis and procedures, pathologic changes, and diseases and signs. For each clinical finding, the user would first select one of the Effect areas. If the user selected Laboratory, they were presented with a menu of sample matrix options which served as the Site. The Laboratory Effects were selected from portions of the SNOMED/SNOVET Functions and Procedures axes. If the user selected an Effect other than Laboratory, the Site would be selected using a modification of the SNOMED/SNOVET Topography axis. The vocabulary for pathologic findings was drawn from the SNOMED/SNOVET Morphology axis and the vocabulary for the disease, sign, syndrome, and abnormal function terms were drawn primarily from the SNOMED/SNOVET Function and Disease axes. A body system code derived from the modified Topography axis was used as well.

We created a separate SNOMEDVET database to hold the unmodified SNOMED and SNOVET terms. From this database, useful terms were extracted for use in the TKS clinical findings vocabularies.

4.2.5 Chemical Name Controlled Vocabulary

The Registry of Toxic Effects of Chemical Substances (RTECS), prepared by NIOSH was to serve as the controlled vocabulary for chemical names. Our goal was to have the RTECS data on-line as a look-up system for the toxic and therapeutic agents entered in the exposure regimen. Unfortunately RTECS is an extremely large system and could not be incorporated within the TKS database structure.

We decided to create a separate RTECS database with rudimentary screen access. The chemical table contained 96,724 rows, the chemical synonyms table contained 247,072 rows, and the toxic effects tables had 229,466 rows. The size of these tables made on-line functionality nearly impossible. A query using a synonym required up to five minutes to complete. Although the retrieved data was useful, the overall slowness made the RTECS unsuitable for the purposes we intended. Because of this, we planned to develop a separate chemical controlled vocabulary table which would hold selected chemicals from the RTECS files and other information sources. As a smaller table within the TKS system, it would be more responsive and could hold other useful information such as the reprint filing system information. We were unable to complete this component by the end of the project.

4.3 User Application

The user application is how the user interacts with the underlying Toxin Knowledge System components. Through the application, the user can review, add, and modify the standard nomenclature data tables. It also guides the user through the structured abstracting process and subsequent structured monograph generation. Because the application is

essential for the effective use of the Toxin Knowledge System, it was the focus of much of the Toxin Knowledge System development.

The two main actions of the application were to communicate with the user and to communicate with the database. Because of the inherent complex relationships between the various data tables, the user could easily make a mistake in data entry that would drastically impact the TKS operations. The database tables relate and interact in a myriad of ways, much like a spider's web. We believed the user should be able to use the application with limited effort needed to maintain the "spider's web." The application should make or break the connections as needed. If a change is made in one table that affects another table, the application should display the appropriate means for either monitoring the change or adjusting the table data. We wanted the application to maintain the inter-table relationships invisibly and with no input from the user. The application should also react to the data that the user enters to direct the structured abstracting process.

The application should use a combination of menus and windows to communicate with the user. Informix-4GL® provides the tools to rapidly implement windows and "ring menus" (i.e., menus like Lotus 1-2-3®). Informix-4GL® does not provide for drop-down and hierarchical menus which we would have preferred. As new functions were added to the application, we were able to quickly incorporate them in to the menu structure. When the application contained about 75% of the functions, we had to revise the menu structure to better integrate the menu choices and make the overall flow easier to follow. This revision put similar procedures together. The menu titles were revised to have unique identifiers, further facilitating the users movement within the system. The revised menu system is depicted in Appendix D. An example of the menu changes was our putting all the "Add" functions under one menu and the "Find" functions under another. While this was generally less confusing, it was awkward to move between the "Add" menu and the "Find" menu, although this movement was frequently necessary. This was resolved by adding a mechanism to jump from one menu to the other without the usual maneuvering through the menu tree.

Some modules make extensive use of context sensitive pop-up options to guide the user. We used codes for all columns that would use the pop-up option and used an associated translation function to display the meaning of the code to the screen. Because the same translation functions were used to convert the codes for use in the monographs, the user saw the words that would be in the monograph as he/she selected the most appropriate pop-up choice.

Because the application would direct the flow of the user's interaction, it was important to communicate to the user where they were within the application. This involved consistently labeling the data entry screens so that the casual or infrequent users could know which table was being accessed or the function executed. Similar labels were placed on the menus. A more significant addition was the inclusion of on-line help screens into the application to provide context-sensitive assistance throughout the application.

For the user to find data within the system, we utilized "Query-by-example" search strategy in association with the data entry screens. This would permit the use of "wild-cards" to find terms. Once the user's query was complete, the application used a "Browse" menu to let the user page through the retrieve information. This "Browse" menu also included a "Query-Again" option to readily permit additional searches. The "Query-by-

example" approach generally retrieves data from one database table. This did not permit the user to see related data in other tables. To resolve this, we developed and incorporated a "top-down" query mechanism which allows a user to query on any single table and rapidly see the associated data in all other tables. This mechanism did not permit cross-table queries but did allow a user to enter search criteria and find the needed data. We also added summary fields to the citation and paper overview screens to show the number of records in each linked table.

TKS had been designed with the primary key being a citation number derived from the journal, volume, page, and year. This provided a unique number for identifying the paper. A citation file number was added to the system for internal filing purposes. With increased use, we found that the citation file number was easier to work with than the citation number. As papers were entered into the citation component of the system, the citation numbers were assigned. Users trying to add content data from a specific paper to the system had a copy of the paper in hand but could not readily derive the citation number from the paper alone. To overcome this we developed a mechanism for the user to enter the author, volume, page, and year information from the actual paper and access detailed information within the system. This mechanism was based on a revision of the citation file number format.

4.4 Structured Abstracting Process

The structured abstracting process uses windowed data entry screens to ask the user for the needed information. Depending on the information entered, the application will generate needed codes, validate the data entered and give feedback to the user, select the options to be displayed on screen, and choose the next screen for data entry. The following section shows the flow and background of entering a new paper into the TKS system.

4.4.1 Citation Table

The citation of any piece of scientific information is the primary identifier and as such is the primary entity in the TKS entity-relationship model. Many citation based systems focus only on journal citations; however, we found this to be a restrictive approach. After analyzing the components of journal and book citations, we were able to identify similar elements which could be extracted to become the identifying data for a given citation. We put these elements into the citation table and the journal or book specific information became a part of the journal or book vocabulary. The citation table would serve as the master table for all subsequent data tables. The citation would link to the journal or book reference via the citsource column. Other data tables would link to the citation table using a citation code number created when the citation is first entered into the Toxin Knowledge System.

When the user first accesses the data entry screen, a window opens and prompts the user for the first author's last name. Subsequently, the main data entry screen for this table opens and is shown below in Figure 1.

```

Enter source code OR journal> F5/Cntl-F, book> F6/Cntl-B, Help> Ctrl-w.
                                CITATION DATA SCREEN
Citation No: [ ] File No: [ ]
Source: [ ] File Loc.: [ ] Entry Date: [11/02/1990]
Volume/Chap: [ ] Pages: [ ]-[ ] Year: [ ]
Title:
[ ]
[ ]
[ ]
[ ]

Journal/Book Title:
[ ]

Authors [0 ] Keywords [0 ]
PaperOver [0 ] Designs [0 ] Subjects [0 ] ExpoRegm [0 ] Signs [ ]

Help is available. Hit Ctrl-W for help.

```

Figure 1. Citation Data Entry Screen

At first the cursor is in the Citation Source field and a message indicates that journal sources and book sources are available for look-up at the press of a function key. Figure 2 shows an example of the journal look-up screen. Depending on the function key selected, the user can query for a journal abbreviation or book title using wildcard searching. Up to thirty entries meeting the search criteria are displayed in the window. The user can scroll through these entries and select the desired journal or book by pressing the Escape key. The look-up window disappears, the selected journal or book code is automatically inserted into the Citation Source field, and the journal abbreviation or book title is displayed for verification. The user can elect to change this entry by entering a different number or pressing the look-up function key again.

Enter source code	J-LIST: Find Add Select Exit	
	Highlight a journal abbreviation and press ESC	
Citation No: []		JOURNAL SOURCE LIST
Source: []	[FUND BANK REV FINANC DEV] [J02617]
Volume/Chap: []	[FUND RAISING MANAGE] [J02618]
Title:	[FUNDAM APPL TOXICOL] [J00001]
[]	[]] []
[]	[]] []
[]	[]] []
[]	[]] []
[]	[]] []
Journal/Book Title	[]] []
[]	[]] []
[]	[]] []
Authors [0] K	[]] []
PaperOver [0] D	[]] []
[]	[]] []
[]	[]] []

Help is available. Hit Ctrl-W for help.

Figure 2. Journal Look-up Screen

After the Citation Source entry, the user continues to enter appropriate data into the screen entries. See Figure 3 below for completed screen. When all of the appropriate data is entered, s/he pushes the Escape key, the data is inserted into the citation table in the database, and the author entry portion is called.

An indication of the application's role in the structured abstracting process is seen in the generation of access coding. The primary access code was designed to be the citation number which is generated by the application. After the year value is entered, the the citation code number is generated and put in the corresponding field. The format for the code number is J/BSSSSS-VVVV-PPPPP-YYYY where J or B indicates whether it is from a journal or book, SSSSS indicates Citation Source value, VVVV is the volume/chapter number, PPPPP is the first page number, and YYYY is the year. For example, a citation from *Fundamental and Applied Toxicology*, volume 9, pages 588 to 594, published in 1987 would have the following citation code number: J00001-0009-00588-1987. The zero padding was required and managed by the application automatically. The citation file coding system was developed to assist users trying to add content data from a specific paper to the system. Generally the user had a copy of the paper in hand but could not readily derived the citation number from the paper alone. The citation file number was automatically generated by the application. The citation file number format was AAAA.V.P.YY where AAAA is the first four letters of the first authors last name, V is the volume number, P is the page number, and YY is the last two digits of the year.

Enter source code OR press F5 for journal, F6 for book help.

CITATION DATA SCREEN

Citation No: [J00001-0029-00588-1987] File No: [BEAS.9.588.87]

Source: [J00001] File Loc.: [3P] Entry Date: []

Volume/Chap: [3] Pages: [588]-[594] Year: [1987]

Title:

[DISTRIBUTION OF BLOOD FLOW TO THE GASTROINTESTINAL TRACT OF SWI]

[NE DURING T-2 TOXIN-INDUCED SHOCK]

[]

[]

Journal/Book Title:

[FUNDAM APPL TOXICOL]

Authors [4] Keywords [7]

PaperOver [1] Designs [0] Subjects [3] ExpoRegn [3] Signs[1]

Help is available. Hit Ctrl-W for help.

Figure 3. Completed Citation Data Entry Screen

As more papers were entered into the system, an increasing number of duplicate papers were found. We identified three situations where duplicate entries arose. One was a second copy of a previously entered paper. This situation could be handled by either ignoring the second copy or by updating the original entry as needed. The next situation was from keyboarding errors, which could be managed by correcting the erroneous information. The third and most difficult situation to manage were circumstances in which two papers actually have the same journal citation information. Examples of this are letters to the editor or abstracts in proceedings. We provided for a sequencing number to be added to the end of the citation number.

4.4.2 Author Table

Immediately after the Citation data has been accepted by the user, the Author entry window appears. Because the number of authors varies, we used a separate table to hold the author names and their order of authorship. Each entry was joined to the other tables via the citation code number. The entry screen for this table is shown in Figure 4 below. The citation code number is automatically displayed to assure correct links to the citation table. The user enters the authors' names into a scrolling entry array. Assuming the names are put into the system in order, the program will automatically generate the publication order number as the user puts additional names into the array. The current system allows up to 20 authors' names to be entered. Each author entry has a serial number assigned but it is not displayed.

CITATION DATA SCREEN

Citation No: [00001-0009-00588-1987] File No: [BEAS 9 588 87]
 Source: [000001] File Loc.: [BP] Entry Date: []
 Volume/Chap: [2] Pages: [588]-[594] Year: [1987]
 Title:
 [DISTRIBUTION OF BLOOD FLOW TO THE GASTROINTESTINAL TRACT OF SWI]
 [NE DURING T-2 TOXIN-INDUCED SHOCK]

AUTHOR DATA SCREEN

Citation: [00001-0009-00588-1987] Citfile: [BEAS 9 588 87]
 Author:

	AuthSig:
[BEASLEY UA]	[1]
[LUNDEEN GR]	[2]
[POPPENGA RH]	[3]
[BUCK WB]	[4]

Hit ESC to leave array.

D
K,

Figure 4. Author Data Entry Screen

4.4.3 Keyword Table

Toxin-related articles were entered into Toxin Knowledge System citation tables before the paper content tables were implemented. If the users were to have effective management of these citations, a mechanism other than the title had to be used. We decided to add a keywords table and associated keyword list table to the system. As mentioned above Appendix C contains the keywords used. We originally planned to eliminate this table when the Toxin Knowledge System was complete. Late in the project, we began to appreciate the simplicity of the keyword approach and began to study ways that the application could automatically create keywords from the data entered in the structured abstracts. This was not completed.

After the user enters the citation and author data as described above, the keyword module is activated to permit entry of up to 20 keywords. The screen used to enter this data is shown in Figure 5.

The screenshot displays a terminal window titled "KEYWORD DATA SCREEN". On the left, there is a form for entering citation and author data. On the right, there is a list of keywords with corresponding codes.

Citation Information:

Citation No: [000001-0009-0]
Source: [000001] File
Volume/Chap: [8] Page
Title: [DISTRIBUTION OF BLOOD F
[NE DURING T-2 TOXIN-IND

Author Information:

Citation: [000001-0009-00]
Author:
[BEASLEY UA
[LUNDEEN GR
[POPPENGA RH
[BUCK WB
Hit ESC to leave

Keyword List:

Key Code	Keyword
[014	[RADIOLAZEL
[A05	[BLOOD FLOW
[E03	[YOUNG
[D02	[FEMALE
[C05	[SWINE
[Q03	[TOX IN VIVO
[A03	[T-2
[[
[[
[[
[[

ESC to continue

Figure 5. Keyword Data Entry Screen

The data entered is compared to a list of accepted keywords in the keylist table. This table is used for verification and on-line look-up. The interactions between the keywords table and the keylist table are depicted in Appendix A. Users can either input a code and the application will look up and insert the corresponding keyword or they can input a keyword and the corresponding code will be determined and inserted. This dual mechanism was found to be more effective than having only one mechanism. Users find that

there are certain keywords that are frequently used. If they learn the code for these words, three keystrokes produce a keyword that would require up to 20 keystrokes. Infrequently used terms might be remembered as words but not as the associated codes. The TKS application addresses both situations.

4.4.4 Paper Data Processing

After the citation, author, and keyword data have been entered, the application focuses on the paper's content. Because the interactions of study design, subject characteristics, exposure regimens, and results are inherently complex, the database design for the data tables was complex as well. The paper content is divided into four larger sections: Paper Overview, Methods and Materials, Results, and Discussion and Comments.

4.4.4.1 Paper Overview Section

The paper overview section is the master section for all content sections in the Toxin Knowledge System and consists of a single database table, *paperover*. The contents of this table are presented in Appendix B. Appendix A shows the interactions this table has with the tables in the Methods and Materials Section and the Results Section.

For each paper there is only one entry in the *paperover* table. It serves as a foundation for the multiple entities in the other content tables. In addition to the table-to-table linking information, this table contains certain basic information about the paper. Both the stated purpose of the paper and the abstractor's impression of an implied purpose are collected and stored here. An implied purpose can frequently give insight into the authors' biases that might be at work. This table also contains the aim of the paper based on a list of acceptable terms for this item. Data entered in this table provided the foundation for application-directed abstracted. After the abstractor indicates the number of designs in this table, the application controls how many study designs can be entered in the Materials and Methods Section. The data entry screen for this table is shown in Figure 6.

The user's interaction with the above screen is straightforward. When a new citation is entered into the system, the citation number and citation file number are carried over from the citation entry process. When the user intends to add content data for a citation already in the system, s/he will be prompted for the citation number or citation file number for the entered paper. Regardless of the access point, these numbers are put into the corresponding fields on screen. The user enters the purpose data and selects the desired aim or paper class from the choices available. After entry of the code number, the associated translation appears next to it. The user then enters the number of study designs in the paper. The system supports up to 99 study designs. For example, if the paper consists of a case report of a human exposed to a toxin and an animal study to replicate the effects seen in the human, there would be two study designs and a 2 would be entered in the screen field. After all the data is entered, the user pushes the Escape key and the data is inserted into the database. If this is the entry of a new citation or if the entry for the number of designs has increased, the user will automatically go to the study design screen.

PAPER OVERVIEW SCREEN	
Citation Num: [J00001-0009-00588-1987]	File No: [BEAS 9.588.87]
[1]	
Stated Purpose: [STUDY GASTROINTESTINAL BLOOD FLOW IN T-2 TOXICOSIS]	
Implied Purpose: []	
Paper class: [] [E10] [EXPER-TOXICITY]	
Number of Study Designs in Paper: [2]	

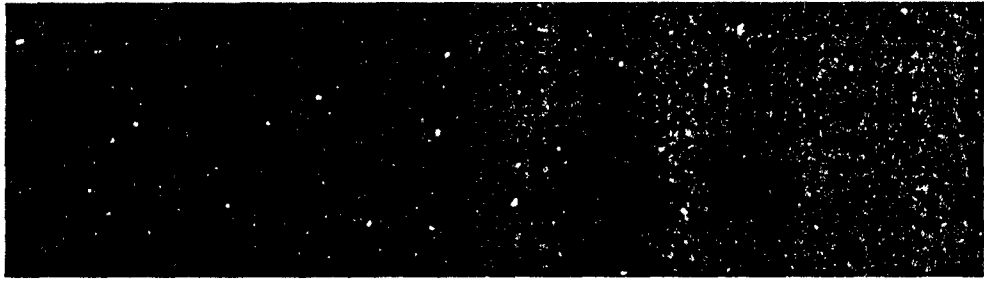


Figure 6. Paper Overview Entry Screen

4.4.4.2 Methods and Materials Section

In keeping with the standard style for writing scientific papers, the Methods and Materials section contains the data tables needed to hold data about the various methodologies and materials used in the study. These tables hold study design (*studydsgn*), subject groups (*subjgrp*), exposure regimens (*exporegm*), and exposure groups (*expogrp*).

4.4.4.2.1 Study Design

The data table *studydsgn* contains the general design information, the controlling technique data, the number of subject groups involved in this design, and the number of exposure regimens in this design. This table is described in detail in Appendix B. The number of entries permitted in this table is controlled by the number of designs entered in the *paperover* table. The data entry screen for this table is shown in Figure 7.

```

Hit RETURN to begin to add data.

Citation No: [000001-0009-00588-1987] File No: [BEAS 9 588 87] Design No. [1] of [1]
Type of Study: [3] [EXPERIMENT]
In Vivo o In Vitro: [0] [IN VIVO]
Controls (y/n): [0]
Comparison Info: [1] [BETWEEN GROUP]
Comparison Methods: [2] [PARALLEL GROUP]
Control Methods: [1] [CONCURRENT]
Control Types: [2] [NO AGENT]
How where subjects assigned to their groups? [ ] [ ]
Numb. of Subject Groups: [ ]
Numb. of Exposure Regimens: [ ]

```

A = Randomized
B = Matched Pair
C = Arbitrary Assignment
N = None
U = Unknown

Figure 7. Study Design Data Entry Screen

Each entry is automatically assigned a serial number which is used by the application to link this table to the corresponding subject groups, exposure regimens, and exposure groups entries. When the screen opens, the citation number and the citation file number are filled in. The total number of designs is also indicated (passed in from the paperover table) and the design number for this design. In Figure 7, the entry is the first and only design. If there were 4 designs in the paper, the entry might read "Design No. 2 of 4". These values are maintained by the application. The first entry that the user/abstractor makes the Type of Study. (See Appendix G. Documentation for more detailed information about the choices for each field.) As the user moves the cursor through the entry fields, pop-up choices appropriate for that field appear. In Figure 7, the cursor is in the subject assignment field and 5 choices have appeared. After the user enters the code for a selection, the translated term appears to the right of the code. For example, the Type of Study code is "B" which is translated as "Experiment". When the user enters the number of subjects, the subject group data entry screen appears. After all subject groups have been entered, the user returns to the study design screen to enter the number of exposure regimens. With the entry of this number, the exposure regimen data entry screen appears for entry of all of the exposure regimens in this design. After all exposure regimens are entered, the user again returns to the study design screen to enter additional study designs as appropriate.

4.4.4.2.2 Subject Group Data

The information about the subjects in the study are stored in the **subjgrp** data table. This data is entered using the screen shown in Figure 8. Pop-up choices are used in this data screen as well. In order to assure consistency in the data collected, we added on-screen weight conversion to change all subject weights to kilograms. After the user enters the initial weight value and units, the program makes the necessary conversion and displayed the changes on-screen. This provided a more consistent way of comparing data in the monographs.

SUBJECT GROUP DATA SCREEN		
Citation No. [000001-0009-00588-1987]		
Group [4] of [3] of Design [1] []		
Species [PORCINE]	Breed [NOT STATED]	Source [NOT STATED]
Number: []		M = Male
Sex: [F] []		F = Female
		C = Castrated Male
		B = Both Sexes
		N = Neutered Female
		U = Unknown Sex
Age: [][] []		
Weight: [][] []		
Height: [][] []		
Occupation (if appropriate): []		
Health Status of Subjects: []		
Total Number of Exposures Received: []		

Figure 8. Subject Data Entry Screen

4.4.4.2.3 Exposure Regimens

Figure 9 shows the data entry screen for the Exposure Regimen data which is stored in the data table **exporegm**. Like the Study Design and Subject Group screens, pop-up choices and on-screen verification are extensively used. We intended for the exposure regimen entry process to utilize the Chemical Controlled Vocabulary to assure that the correct name for the exposure agent was entered. Because of the difficulties in working out an acceptable controlled vocabulary (see above), this function could not be developed.

EXPOSURE REGIMEN DATA SCREEN
[4]

Citation No.: [00001-0009-00589-1987]

Regimen No.: [1] of [] regimens in Study design [1] []

Purpose for Exposure: [TOX] [TOXIC]

Agent: [ETHANOL 70%]

Dose: [7] [ML]

Formulation: [04] [LIQUID]

Route: [18] [INTRA-ARTE]

Interval: [ONCE]

Duration: [ONE DOSE]

Administration Method: [PULMONARY ARTERY (NF)]

Scheduled Evaluation Time: [EVERY 15 HRS]

TOX = Toxic
TRT = Treat
CNL = Control
OTH = Other
NON = None
UNK = Unknown

Figure 9. Exposure Regimen Entry Screen

4.4.4.2.4 Exposure Group Data

After the study design, subject group, and exposure regimen data are entered, the user must create the links between these information sets. This data is stored in **expogrp**. Although the TKS application manages most of the linkages between tables, we could not devise a mechanism to replace the manual creation of these links. The wide variations in study designs precluded making this automatic.

The purpose of the **expogrp** table (described in Appendix B) is to hold the design-subject group-exposure regimen link which is used to connect this information to the results data. In general, the **expogrp** consists of the link code and brief descriptions of the study design, the subject group, and the exposure regimen. The descriptions serve at least two purposes: to give on-screen verification of this information when the results data are being entered, and to provide this information as needed in the structured monographs.

EXPOSURE GROUP LINK ENTRY SCREEN			
Citation Num:	[00001-0009-00588-1987]	[5]
Exposure Group:	[1][1][1][D1.S1.E1]	ExpoGrp [1] of [3]
Dsgn:	[3 GAP, 3 EXP, Y CNTL]		[1] 12]
Subj:	[5 PORCINE, Age: N-AV, Wt: 55 KG, Sex: F, 1 EXP]		[1] 4]
Expc:	[ETHANOL 70%, 7 ML, IA, given ONCE x ONE DOSE]		[1] 4]

1	=ETHANOL 70%, 7 ML IA, given ONCE x ONE DOSE
2	=T-2 TOXIN, 0.6 MG/KG IA, given ONCE x ONE DOSE
3	=T-2 TOXIN, 2.4 MCG/KG IA, given ONCE x ONE DOSE

Figure 10. Exposure Group Link Entry Screen

After the last study design is completely entered, the screen in Figure 10 is opened. The user confirms the citation number and is then presented with descriptions of all the study designs entered for this paper. The application creates the descriptions by extracting data from the `stdydsgr` table. After the user selects the desired study design number, the application places the selected study design description in the appropriate field and then presents computer-prepared descriptions of the subjects involved in the selected design. Choosing the subject group results in the selected subject description being displayed, followed by presentation of similar descriptions for all exposure regimens in this design. In Figure 10, the user has selected design number 1, which is a controlled study involving 3 subject groups and 3 exposure regimens. Subject group 1 was selected. The corresponding description, which indicates that the group consisted of 6 female pigs with an average weight of 55 kg and were exposed once, was put into the subject group description field. The age of these pigs was not presented in the paper, thus the N-AV in the description. The cursor is in the exposure regimen field and the user is to choose between the three exposure regimen options displayed on-screen. From the paper, the user knows that group 1 received exposure regimen 1 and would enter this number. After the exposure option is chosen, the exposure-group link will be created, which in this case would be D1.S1.E1 meaning design 1, group 1, and exposure 1. This number would be difficult to use without the descriptions stored with the link.

A number of significant features were developed for this particular screen and modified for use in other areas of the application. One of the more important features was the automatic generation of the description by the application. This was the forerunner to the monograph generation development. Another feature was the method for paging through up to 99 possibilities on screen. This permits the user to page forwards and backwards as needed to select the desired item. This technique was modified for use in adding data to

papers already abstracted and was the basis for the pop-up choices in the various paper content screens.

4.4.4.3 Results Section

The Clinical Findings Module was a pivotal component of the TKS and the utility of the data entered in this section was dependant on a number of factors. Clinical findings are reported in various ways including text, tables, and graphs. Because the authors of a paper may report a wide range of clinical findings using different terms, an extensive controlled vocabulary was essential. Many different pieces of information must be maraged at this point in the data entry process. The large amount of data that the TKS needed entered necessitated a clear and efficient mechanism for selecting and entering the data. The clinical findings had to be correctly linked to the appropriate study design, subject group, and exposure regimen.

Figure 11 shows the initial clinical findings screen and the type of data to be stored in the clinfir.d database table.

```
Press F7 or CNTL-G to see available Exposure Groups
CLINICAL FINDING DATA SCREEN
Citation Number: [000001-0009-00588-1987] [ ]
Expo Grp: [ ] [ ]
[ ]
[ ]
[ ]
Clinical Finding: Type:[ ] Site [ ] Effect [ ]
[ ]
[ ]
Change          Severity  Units
[ ] [ ] [ ]
Freq          Onset      Duration
[ ] [ ] [ ]
```

Figure 11. Clinical Findings Data Screen (Initial)

After confirming the citation number, the user must identify the exposure group that showed the clinical finding. The user is prompted to press certain keys after which brings up the Exposure Group Selection Window as shown in Figure 12. The user would the cursor down the list and select the appropriate group. The descriptions of the design, subjects, and regimen would be displayed on screen for validation.

Press F7 or CNTL-G to see available Exposure Groups

TKSEXGRP DATA SCREEN	
Citation	
Expo Grp:	Total ExpGrp: [3] Citation Num: [J00000 [-0009-00588-1987-]]
	Exposure Group Code: [01.S2.E2] [4]
	Dsgn: [3 GRP, 3 EXP, Y CNTL]
	Subj: [6 PORCINE, Age: N-AU, Wt: 55 KG, Sex: F, 1 EXP]
Clinical	Expo: [T-2 TOXIN, 0.6 MG/KG, 1A, given ONCE x ONE DOSE]
	Exposure Group Code: [01.S1.E1] [5]
	Dsgn: [3 GRP, 3 EXP, Y CNTL]
Change	Subj: [6 PORCINE, Age: N-AU, Wt: 55 KG, Sex: F, 1 EXP]
[] []	Expo: [ETHANOL 70%, 7 ML, 1A, given ONCE x ONE DOSE]
Freq	Exposure Group Code: [01.S3.E3] [6]
[] []	Dsgn: [3 GRP, 3 EXP, Y CNTL]
1 of 1	Subj: [6 PORCINE, Age: N-AU, Wt: 55 KG, Sex: F, 1 EXP]
	ExUse T-2 TOXIN, 2.4 MCG/KG, 1A, given ONCE x ONE DOSE]

Figure 12. Clinical Findings Screen with Exposure Group Selection Window

One of the most difficult problems we faced in this section was in efficiently accessing the clinical controlled vocabulary. We recognized that the clinical findings data could be classified into three broad areas: pathologic changes, laboratory analysis and procedures, and diseases and signs. After entering the exposure group information, the cursor goes to the Clinical Finding Type field. The user first indicates the exposure and subject group link for the clinical signs. The user then can choose between Pathology, Laboratory, or Signs from a menu.

If the user chooses Signs, the Body System selection window appears, as in Figure 13. The user then chooses the appropriate body system for the sign in question and the TKS Findings Synonym screen appears (Figure 14).

Citation Number:

Expo Grp: [D1.S3
[3 GRP, 3 EXP,
[5 PORCINE, Age
[T-2 TOXIN, 2.4

Clinical Finding:
[BLOOD
[]

Change [] S
[] [] []

Freq [] Onset []
[] []
1 of 1 rows fou

A - Circulatory
B - Digestive
C - Hemato / Lymph / Reticuloen
D - Integumentary / Skin
E - Musculoskeletal
F - Nervous / Behavioral
G - Reproductive
H - Respiratory
I - Senses
J - Urinary
K - General
L - Endocrine
M - Other/Immunologic/Metabol

Z - Exit without choosing
Enter letter for body system >

ING DATA SCREEN

[]

[]

[]

Figure 13. Clinical Findings Screen with Body System Selection Window

By dividing the user's approach to selecting the desired term, we were able to divide the controlled vocabulary into four areas. This approach in conjunction with our developing a two-tiered controlled vocabulary arrangement improved the performance in data entry. The first tier consists of a table of frequently used clinical findings extracted from the second tier SNOMED/SNOVET tables and a synonym table that provides a lookup method for the first tier controlled vocabulary. This is what is shown in Figure 14. The user enters a synonym in the TKS application and the program will search the synonym list for its presence. If the desired term is not present in the first tier vocabulary, the user can move to the second tier to search for and extract the desired term into the first tier if needed. The second tier system is a modification of the current methodology for selecting clinical findings. The relationships between the various vocabulary tables and the clinical findings table are shown in Appendix A.

Clinical Finding Synonym
[CARDIAC*

TKS FINDING SYNONYM SCREEN

[A01962] [CARDIAC DYSKINESIA
[A02172] [CARDIAC DYSRHYTHMIA, NOS
[A01966] [CARDIAC EJECTION FRACTION
[A01967] [CARDIAC END DIASTOLIC VOLUME
[A01980] [CARDIAC FLOW, ABNORMAL, NOS
[A01979] [CARDIAC FLOW, NORMAL
[A01978] [CARDIAC FLOW, NOS
[A01957] [CARDIAC FUNCTION, ABNORMAL
[A01960] [CARDIAC FUNCTION, DECREASED
[A01959] [CARDIAC FUNCTION, INCREASED
[A01956] [CARDIAC FUNCTION, NOS
[A01958] [CARDIAC INSUFFICIENCY
[A02352] [CARDIAC MURMUR, NOS
[A01970] [CARDIAC OUTPUT, DECREASED
[A01969] [CARDIAC OUTPUT, INCREASED

Searching....

Figure 14. TKS Findings Synonym Screen (Sign Selection)

After the clinical finding is selected from the controlled vocabulary, the user returns to the Clinical Findings Screen where the selected body system and clinical finding is shown. The user then enters the semiquantitative changes, incidence information, and time factors. The completed clinical findings screen is shown in Figure 15.

Citation Number: [J000001-0009-00538-1987]		CLINICAL FINDING DATA SCREEN [133]
Expo Grp: [D1 S3 E3] [6]		
[3 GRP, 3 EXP, Y CNTL]		
[5 PORCINE, Age: N-AU, Wt: 55 KG, Sex: F, 1 EXP]		
[T-2 TOXIN, 2.4 MCG/KG, IA, given ONCE x ONE DOSE]		
Clinical Finding: Type: [3] Site [A] Effect [A01970]		
[CIRCULATORY]		
[CARDIAC OUTPUT, DECREASED]		
Change	Severity	Units
[3] [INCREASE]	[20]	[ML/MIN/KG]
Freq	Onset	Duration
[AVERAGE]	[BY 6 HR]	[NOT APPL]

Figure 15. Clinical Findings Screen (Completed)

If the user had chosen Laboratory Test as the Clinical Finding Type, a slightly different entry process is used. First a sample matrix menu is presented (Figure 16). The selected matrix is used as the site in the clinfind table.

Press F7 or CNTL-

Citation Number:

Expo Grp: [D1.S3
[3 GRP, 3 EXP,
[5 PORCINE, Age
[T-2 TOXIN, 2.4

Clinical Finding:
[]

Change [] [] S []

Freq [] Onset []

1 of 1 rows fou

ING DATA SCREEN

A - Blood
B - Plasma
C - Serum
D - Milk
E - Saliva
F - Gastric Cntnt
G - Feces
H - Vomitus
I - Urine
J - CSF
K - Other Matrix

→ Exit w/o Select

Enter letter for sample matrix >

Figure 16. Clinical Findings Screen with Lab Matrix Selection Window

After the matrix is selected, a list of laboratory test categories is presented as in Figure 17. This categorization facilitates the selection of the actual laboratory test via a screen similar to that in Figure 14.

Clinical Finding
[]

ING SYNONYM SCREEN

A - Elements/Ions/Inorganics/Acid-Base
B - Simple Organics/Carbohydrates
C - Proteins/Amino Acids
D - Fatty Acids/Lipids/Lipoproteins
E - Porphyrins/Bilirubin Cmpd/Bile Acid
F - Purines/Pyrimidines/Nucleic Acids
G - Vitamins
H - Hemoglobins
I - Enzymes
J - Endocrine Substances
K - Nervous System Substances
L - Immune System Substances
M - Hematopoietic Functions

→ Exit without choosing

Enter letter for lab test category >

Figure 17. Clinical Findings Screen with Lab Test Group Selection Window

If the user had chosen Pathology as the Clinical Finding Type, the exact site of the pathologic lesion would be identified. This identification and selection process would use the Body System Selection window (Figure 13) and the TKS Site Selection Screen (Figure 18). The user first selects the Body System and is then presented with the organs within the selected system. After the organ is selected, the exact sites within the organ are presented. With the selection of the specific site, the site code and site description are inserted into the clinical finding screen.

```

System: [3] Organ: [32] Location: [ ] ==> TKS Site: [ ]
[HEART]
[+] [ ]
[32010] [ ] RIGHT SIDE OF HEART [ ]
[32020] [ ] LEFT SIDE OF HEART [ ]
[32030] [ ] BASE OF HEART [ ]
[32040] [ ] APEX OF HEART [ ]
[32041] [ ] NOTCH, APEX OF HEART [ ]
[32050] [ ] STERNOCOSTAL SURFACE OF HEART [ ]
[32060] [ ] DIAPHRAGMATIC SURFACE OF HEART [ ]
[32070] [ ] PULMONARY SURFACE OF HEART [ ]
[32080] [ ] RIGHT MARGIN OF HEART [ ]
[32090] [ ] LEFT MARGIN OF HEART [ ]
[32100] [ ] ATRIUM, NOS [ ]
[32110] [ ] AURICULAR APPENDAGE, NOS [ ]
[32120] [ ] INTERATRIAL SEPTUM [ ]
[32130] [ ] FORAMEN OVALE, NOS [ ]
Use arrows to scroll up and down. Press ESC to select item.

```

Figure 18. TKS Site Selection Screen for Pathology Findings

4.4.4.4 Discussion and Comments Section

The discussion section of scientific papers was difficult to manage within the TKS concept. While the structure of a scientific study provides the structure for much of a scientific paper, the discussions section is generally freeform. We conceived a method to manage the discussion data which would have had much broader applicability to the overall system. The concept would have permitted the inclusion of both comments about the paper being abstracted as well as the authors' comments about a previously published paper. Authors of scientific papers frequently compare their design, results, and conclusions to previous papers. They may state how their work supports, refutes, expands, or explains the previous work. The earlier design or work may be criticized or praised. All of these comments combine to provide a form of running commentary on a paper after it is published.

We designed a Comment table in the TKS database. Data in this table would have included the comment and the area of the paper involved. We had hoped to have comment creation accessible at any entry module in the system. By pressing a function key, the comment entry screen was to appear, allowing the abstractor to include their observations

in the comments table. We had hoped that the experience we gained in putting on-line helps throughout the application would have provide a means of accessing the comments files wherever needed. Unfortunately the programmer responsible for this area resigned and could not be replaced; thus, this section was not completed.

4.4.5 Cross Table Query Process for Keywords and Citations

In the first year of the contract we developed a query-by-example portion of the application to permit screen-oriented multi-table queries of the citation, author, and keyword tables. This screen is shown in Figure 19 below.

QUERY-BY-EXAMPLE DATA SCREEN					
Citation Number: [File Code: [
Journ/Book Code	Vol	Pages	Year	Location	
[[[[[
[
Title of Article or Chapter: [
[
[
[
----- Author -----					
[
[
----- Keyword -----					
[
[
Keycode [][][][

Figure 19. Cross-Table Query-by-Example Screen

The program queries for entries in all three tables which meet the appropriate search criteria. The program concatenates the author and keyword entries into character strings and displays them in the appropriate fields on screen. Figure 20 shows the results of such a query. Using the menus, the user can browse through the citations and elect to output all or selected citations to either a file or to a printer. The output resembles a list of bibliographic citations sorted by the first author's last name.

```

BROWSE: Next Previous First Last Output Exit
View the next Citation in the list.

                                QUERY-BY-EXAMPLE DATA SCREEN
Citation Number: [J00001-0009-00588-1987] File Code: [BEAS.9.588.87]
Journ/Book Code   Vol      Pages      Year      Location
 [J00001]         [9]      [588-594]  [1987]    [BP]
[FUNDAM APPL TOXICOL]

Title of Article or Chapter: [DISTRIBUTION OF BLOOD FLOW TO THE GASTRO]
 [INTESTINAL TRACT OF SWINE DURING T-2 TOXIN-INDUCED SHOCK]
 [ ]
 [ ]

----- Author -----
[BEASLEY JR, LUNDEEN GR, POPPENGH RH, BUCK WB]
[ ]

----- Keyword -----
[RADIOLABEL, BLOOD FLOW, YOUNG, FEMALE, SWINE, TOX IN VIVO, T-2]
[ ]

Keycode [ ] [ ] [ ] [ ]
1 of 1 rows

```

Figure 20. Cross-Table Query-by-Example Results

This module was very effective when searching for one term from each table; however, it would not produce correct results when more than one keyword or author was entered. This problem had two origins. One is fundamental to the relational model in that a Boolean "AND" within a table gives a negative search. A single entry in a table cannot two values. Using the Informix-SQL® query language, this can be overcome using a "UNION" statement in a select statement. Unfortunately the Informix-4GL® "CONSTRUCT" statement, the standard method for preparing query-by-example search procedures, did not permit the use of "UNION" within the query. We were not able to correct this problem by the end of the contract as it was of a less critical nature than the other modules of the application.

4.5 Structured Monograph

The Monograph Generation Module development was hampered by delays in finalizing the paper content components. We could do little effective work in this area with limited or incorrect data in the results tables. In spite of the significant delays, we were able to begin two basic monograph components.

The Monograph Generation Module consisted of a paper abstract component, a generic toxicant oriented component, and a bibliography generation component. The bibliography generation component permits a user to generate a bibliography for every paper in TKS, a given author, or a given generic. This function is automatically called to provide full citations for the generic toxicant abstracts. While the remaining structured abstracting components were being developed, the TKS Library Clerk found and entered almost 2500 citation into the TKS system. The application generated bibliography for these citations are presented in Appendix E.

One monograph component was the paper abstract which generates a monograph showing the entered data for a given paper. This monograph or "structured abstract" allows the user to compare the generated abstract and the original paper. These abstracts were used to identify mechanisms to improve the monograph program. The initial work with the monograph pointed out certain areas within the application we had revised to enter and maintain appropriate data for incorporation within the monograph. We determined that if all the entered data were entered in upper case and computer generated text were in lower case, the reader of a monograph could easily distinguish the paper data from the application data. This necessitated revision of several components of the application, primarily in the paper content sections. This also pointed out several wording problems that were largely the result of the translation functions. These were changed. Some other wording functions were not easily changed. Sample monographs from TKS are in Appendix F.

The monographs for generics were much more difficult to develop. We eventually provided the user with 5 different menu choices, of which 2 were completed. The first choice provided is "System-Sign-Species-Dose-Study Design". With this choice, the application generates a monograph presenting the Sign (clinical effect) grouped by body system and then by the sign. For each sign reported, a paragraph describing the severity and frequency of occurrence in the study group. A description of the subjects, the exposure regimen, and the study design is given, followed by the citation serial number in parenthesis. A reference list of papers cited in the monograph is at the end and arranged alphabetically.

The second choice available is the Total Generic Monograph. This was conceived to be a comprehensive presentation of all data in the TKS for a given toxin. This monograph currently presents a paragraph for each clinical effect seen in each paper entered into the TKS. This paragraph integrates the sign, design, subject, and exposure regimen information into a generally readable form.

Because the monograph is created from the entered data, the quality of the data entry process has major impact on the readability and correctness of the monograph. As we developed the monograph generation module, we became increasingly aware of the inconsistency and omissions in published papers. This created several problems in the TKS design. The entry of data was dependant on the TKS user's ability to translate the authors' statements into our form and terminology. In addition, we needed to have mechanisms to manage situations in which there was omitted data. We were unable to completely resolve these issues before the contract ended.

4.6 USAMRIID Personnel Utilization of System

We anticipated that USAMRIID personnel would utilize the Toxin Knowledge System on the Sequent minicomputer at the UI. As designed an authorized USAMRIID user could dial-up the Sequent computer through a 1200 baud modem or attempt ARPANet access. When the user logged into the Sequent, they would automatically enter a menu-driven program permitting connection to the TKS database. We expected ARPANet connection to serve as the primary means of access as well as providing electronic mail between TKS and USAMRIID personnel. The hardware components to connect the Sequent to the University of Illinois Campus Network were obtained and installed. Through this network, ARPANet connection was possible. Initially there were system software incompatibilities that ham-

pered both remote logins and electronic mail. Although these problems were overcome, USAMRIID personnel experienced performance problems which prevented ARPANet from being an acceptable means for accessing the TKS database. We did not have these performance problems when we accessed other computers via Internet/ARPANet and suspected that the performance problems were located on the USAMRIID computer side.

The USAMRIID personnel requested detailed documentation on the application so that they could more effectively use the system. We prepared the initial documentation on the Sequent but it was later moved to a Macintosh to permit inclusion of graphics, such as screen images and data diagrams. The current version is prepared using PageMaker 4.0 for the Macintosh. This documentation is included in Appendix G.

4.7 Porting TKS To Other Computer Platforms

Although the Sequent computer is an ideal platform for developing Informix applications and maintaining databases. We recognized the need for a "personal" version of the TKS application, a version which one person would use for a more limited set of data. Individuals could benefit by having their own journal selections abstracted into TKS. To achieve this and to make the application more usable for USAMRIID personnel we ported the TKS application to the MS-DOS personal computing platforms.

We obtained Informix-4GL® and the necessary C compiler for this programming environment. Because of limitations in the MS-DOS environment, we chose to use the Informix-4GL Rapid Development System instead. The TKS application was successfully ported to the MS-DOS platform using an IBM PC/AT with 2 megabytes of RAM running the Informix-4GL® Rapid Development System.

5 Discussion of Results

The Toxin Knowledge System was not fully developed during this contract. We experienced a number of setbacks, primarily in programmer support. The principle investigator had to serve as the data analyst, database and application designer, and primary programmer. The programmer hired to assist in this area had limited knowledge of biomedical literature and life science research which proved to be a significant deterrent in her contributing to the overall effort. Her experience in computer system administration was very strong and her primary contributions were in maintaining the computer and network operations. In addition, she left the project early and for the last 12 months of the project all programming and computer support became the responsibility of the principle investigator. In retrospect, it is clear that the project needed at least two programmers for the full length of the contract and that at least one should have had some experience in life sciences. In spite of the problems, development of the TKS proceeded and the results shows some of the promise that a completed system would have.

5.1 Standard Knowledge Structure

The Standard Knowledge Structure developed for TKS primarily covers *in vivo* toxicology testing. It relates the various facets of study design to the clinical problems seen. The structure is sufficiently flexible to permit extensions to cover other areas, such as analytical studies, *in vitro* work, and retrospective studies. We began the analysis for the analytical studies but personnel shortages forced us to abandon it for other more pressing areas.

The comments or discussion section of the Standard Knowledge Structure received considerable attention, but was not implemented. To implement this section, we needed to be able to provide *ad lib* access to the comments data table. This data table would need to have a many-to-many relationship model, which is difficult to execute with traditional relational database systems. By the end of the contract, we had several firm ideas of how to achieve this but did not have the personnel to do so.

5.2 Standard Nomenclature

The development of a functional species independent clinical findings vocabulary was an important step. The multi-tier approach and categorization of clinical findings has proven successful. While the current version of the vocabulary needs to be refined and synonyms added, it provides an excellent base for future work.

Unfortunately, the chemical vocabulary was not successfully developed in spite considerable effort. We believe that a multi-tier approach for this vocabulary would work as well but did not have the personnel to complete this work. The most promising mechanism to provide the chemical vocabulary would have used an "error list" of chemicals entered each day. As the abstractor entered agent data, the application would compare the entered agent against the vocabularies. If the agent were in the vocabularies, the application would proceed normally. If the agent were absent, the user would be prompted for the action to take. If the agent were misspelled the user could change the spelling. If the agent were not in the vocabulary but should be, the agent would be added but also put into the "error list" for periodic review. Initial papers would have taken much more time to enter with this approach, but eventually the vocabularies would contain the majority of the needed terms.

Expansion of the monograph generation functions would have necessitated additional changes in the Study Information Terminology. These changes would have to be made to improve the readability of the monographs, especially as new monograph forms were developed.

5.3 User Application

The user application works well for most situations. Although we would prefer to have drop-down and hierarchical menus instead of the ring-menus that Informix-4GL® provides, the overall functionality is excellent. Additional usage would obviously identify problems with the current programming and new ways to improve the users interaction.

5.4 Structured Abstracting Process

Scientific literature proved to be the most significant obstacle to the structured abstracting process, but the difficulties were enlightening to the abstractors. The TKS standard knowledge structure and corresponding structured abstracting process are based on certain assumptions which frequently were not true. The primary assumption is that the scientific papers are well done. Unfortunately, many authors inadequately describe the studies performed and the results they obtained. It is not uncommon for an author to use several different study designs and compare the results as if they were from a single design. Potentially important information about the subjects is frequently omitted from the paper. Results are difficult to find and/or interpret. The pressure on the authors to publish and the pressure on the journal editors to have papers published is creating a situation that truly needs a system like TKS.

The problems mentioned do not keep TKS from working as designed, but they do make abstracting papers into TKS more time consuming than it should. On several occasions, TKS abstractors would recognize problems with a scientific paper while trying to put it into the system.

Our personal experience and discussions with other scientists suggest that many scientists are unable to fully read many of the papers that they retrieve and that those that are read are not being critically reviewed. Many do not read the papers they collect, but merely file them for possible future use. Some only read the abstracts of the papers which frequently do not accurately reflect the content of the paper.

A system like TKS could provide a more functional access to literature. If a repository of abstracted papers were available, a researcher could tailor their information requests to study design, not just the title of the paper. To do this however would necessitate having abstractors working continuously to maintain the repository which would be beneficial but manpower intensive. This abstracting process is unlikely to be automated because of the myriad of ways that a paper can be written.

We still believe that the concept of structured abstracting is valid and has promise. Perhaps the realization of this promise would be more likely to be seen if researchers were required to "write" their papers in a structured abstract form. This could communicate more than the pages of prose that currently is used.

5.5 Structured Monographs

We had just begun to develop the structured monograph generation modules at the end of the contract. While the current output is not entirely satisfactory, the programs that created them were written in under a day. With additional time and a larger number of papers entered into the TKS, the monographs could become very useful. The monograph forms currently are prose in nature. We think that additional forms, such as tabular output, could provide additional insight and comparison. A significant limitation of the current system is in typographic control. If the system were developed only for UNIX® computers, output controls using the text processing tools such as "nroff" and "ditroff" could be incorporated into the monograph. Better control might be achieved by using PageMaker style flags and downloading the monograph into a PageMaker file for output.

5.6 Comparison of this system with text retrieval systems

In the past year, a number of advances have been made in text retrieval systems which would appear to be more suitable for TKS than a relational database system. Recent articles in trade publications have described these systems along with their strengths and weaknesses. We think that text retrieval systems could be used to extract information for inclusion in TKS, but that the structured storage of data has more comparative and evaluative power than the text retrieval systems. The text retrieval systems are designed to search through large amounts of text for a word or its synonyms. For these systems to be most effective, the synonym listings must be modified for local needs. This is similar to the creation of a controlled vocabulary.

6 Conclusions

The development of the Toxin Knowledge System was intended to provide a tool that would facilitate the acquisition and maintenance of knowledge. Tools are only useful when

they are used. If TKS had been completed, the major difficulty would be the amount of time needed to put the information into the system, yet researchers will overlook needed information, accept as truth the incorrect information in author's narrative abstracts, and fail to compare papers adequately.

While the limitations of scientific literature have been described for decades, few changes have been made in either the editing and publication of the papers or the critical utilization of the published works. The burgeoning amount of information being published makes it unreasonable to expect individual scientists to manage their own information to the extent needed. While it is unlikely, it would appear worthwhile to create and establish more critical information systems to supplement the citation and abstracting systems currently in use. Reporting of biomedical research funded by federal funds should include detailed descriptions of study design and results on abstracting forms that could be easily coded into the these new information systems. This could provide an initial point for controlling the information glut.

The recent developments in imaging and text retrieval systems would appear to provide complimentary technologies to the TKS concept. If articles could be scanned into a computer and stored on optical disk for future review and usage, these could be viewed on screen while entering the data. With new technologies in relational database systems, these scanned images can be stored as a part of the relational database.

7 Recommendations

TKS is a needed tool. We would recommend that TKS be completed and expanded to incorporate new study designs and approaches. A central facility should be established to abstract papers and reports into the TKS. As more papers are entered into TKS, new monograph formats could be designed to better communicate the compiled data. It would seem worthy for USAMRIID to establish new requirements for the reporting of biomedical research to include detailed descriptions of study design and results on abstracting forms that could be easily coded into the TKS database.

**Appendix A.
Graphical Depiction
of
Toxin Knowledge System
Database Design**

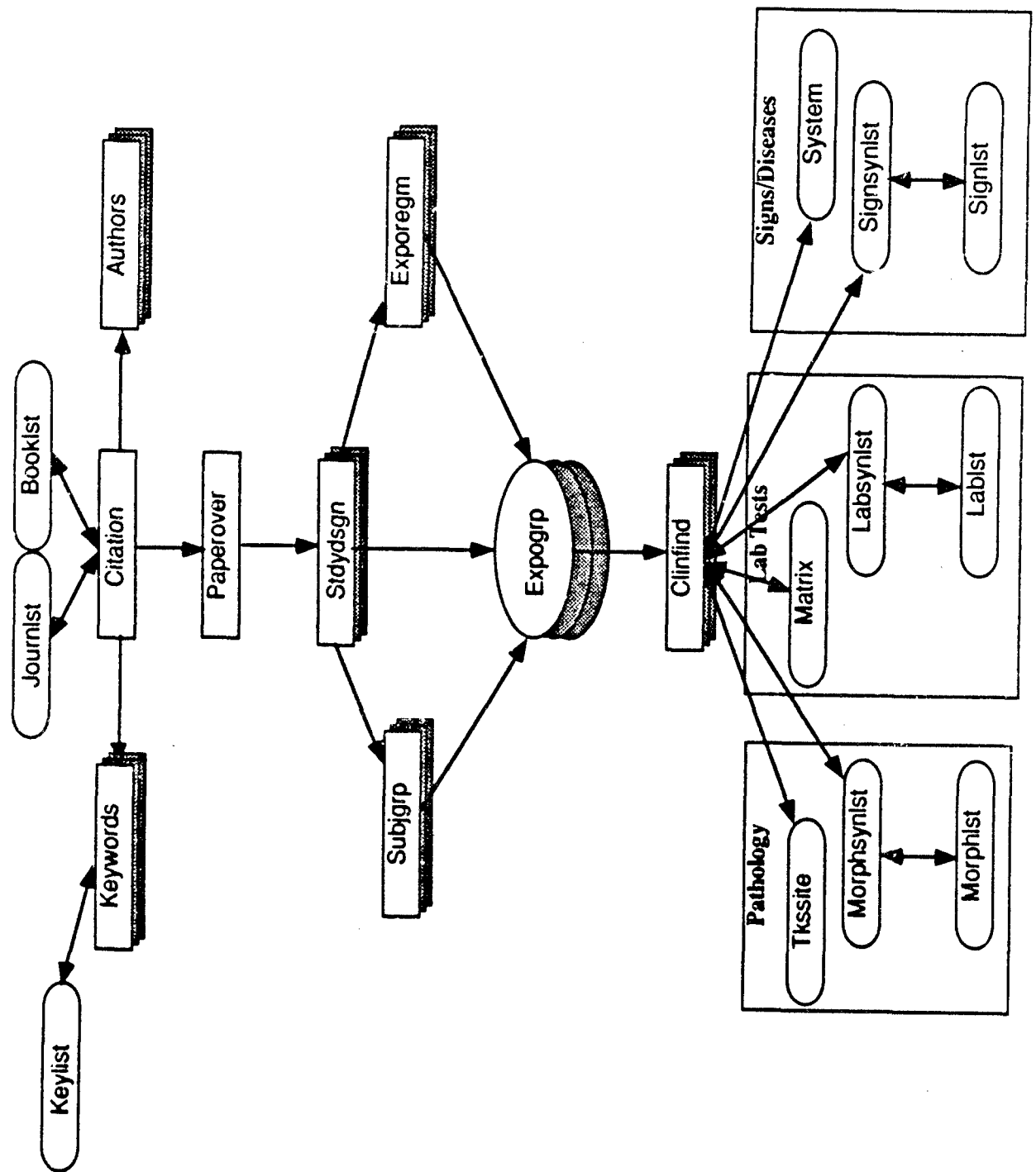


Figure 21. Overview of Toxin Knowledge System Database Design

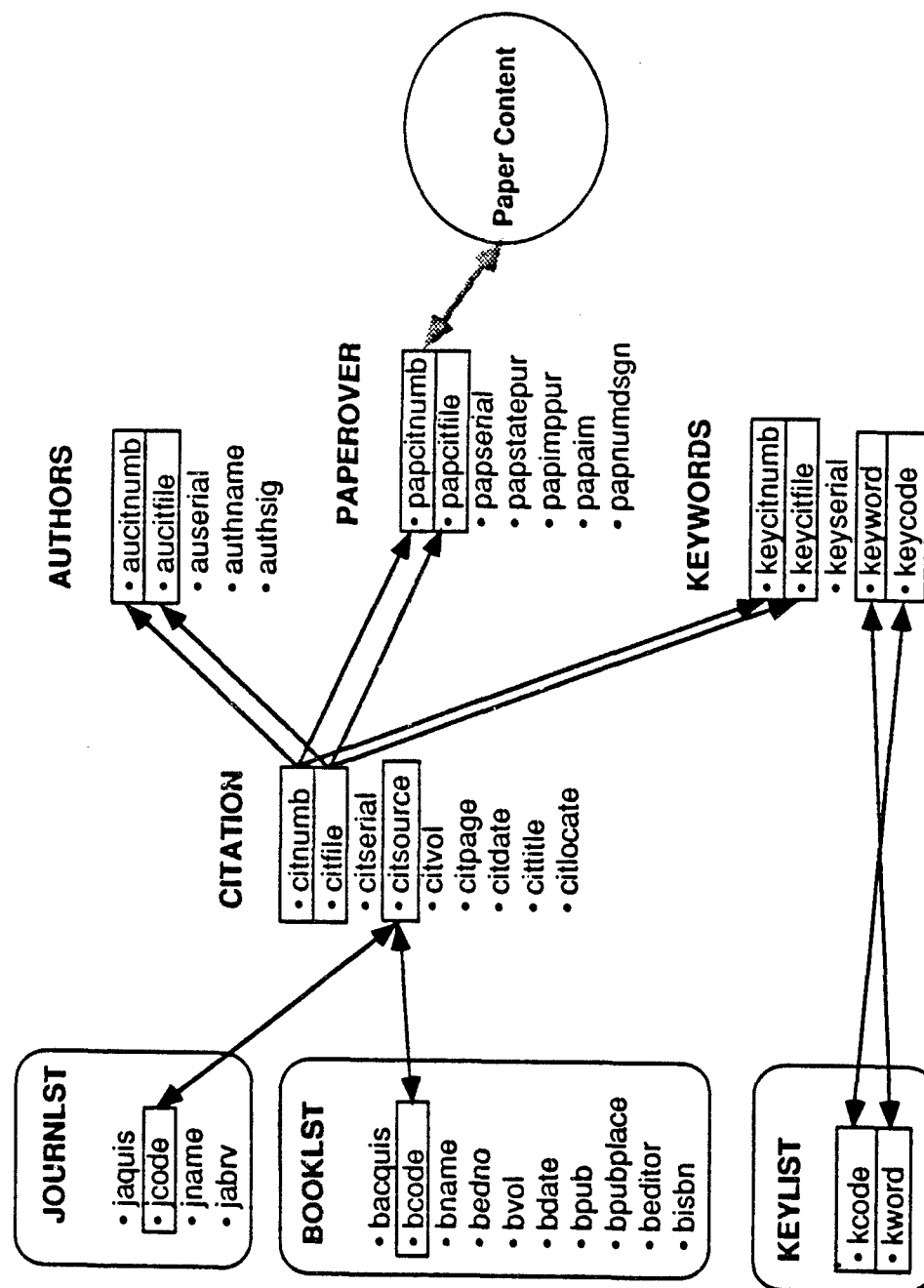


Figure 23. Citation Data Table Interactions

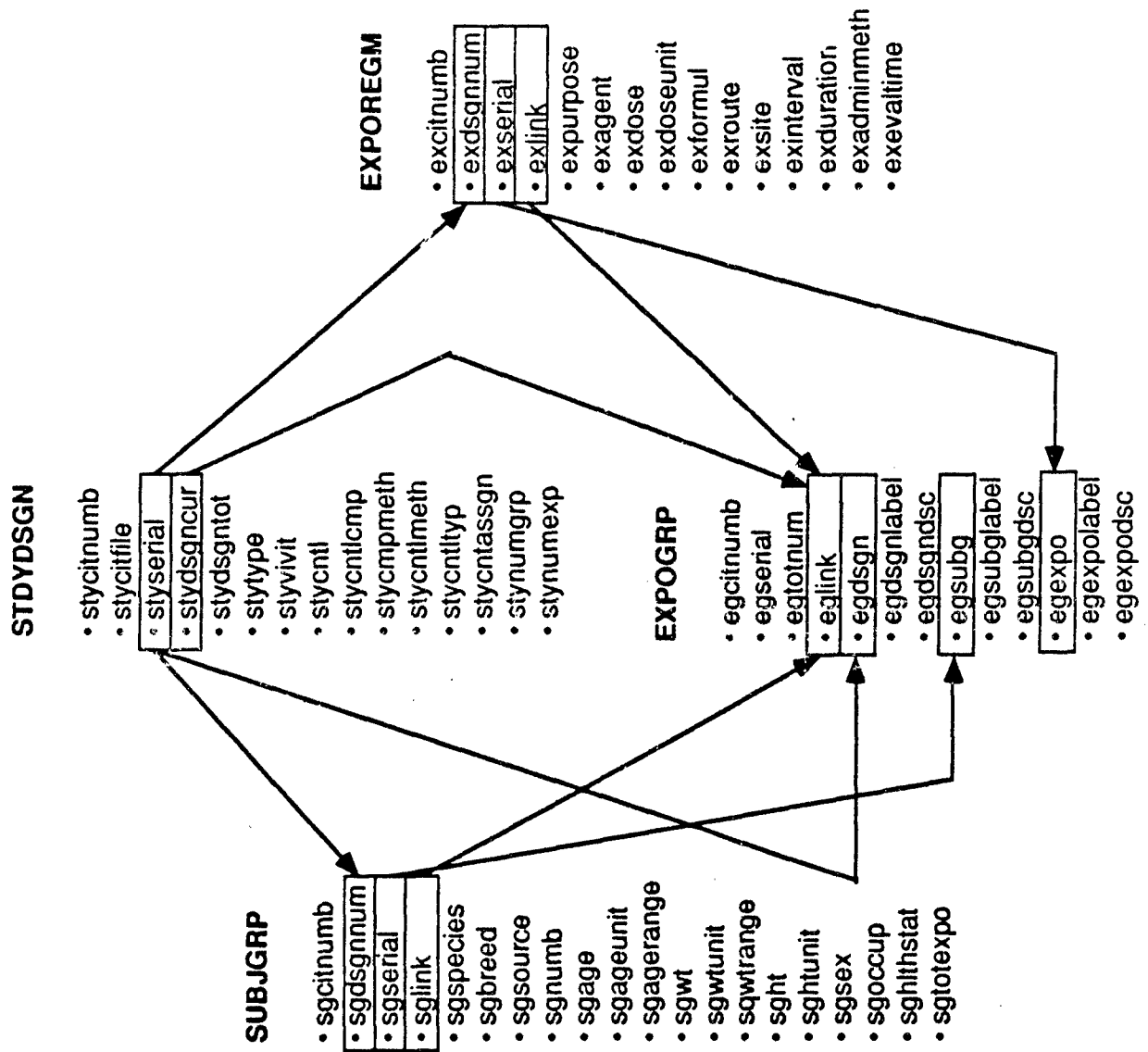


Figure 24. Paper Content Tables Interactions

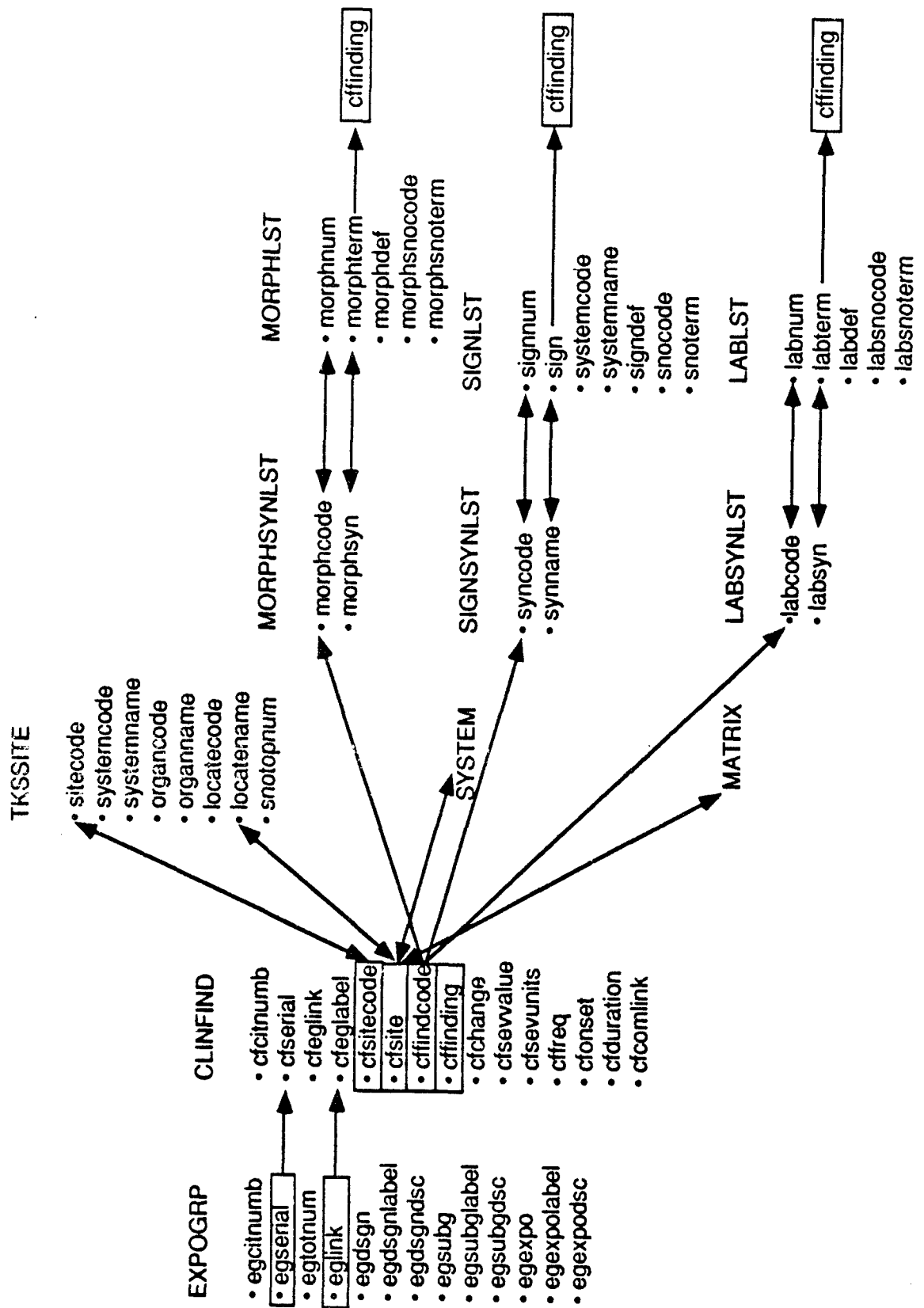


Figure 25. Clinical Finding Table and Reference Table Interactions

**Appendix B.
Textual Description
of
Toxin Knowledge System
Database Design**

Note: Database table names are presented in Helvetica Bold Italic and columns within the table are presented as Helvetica Bold only. General sections of the database are presented as Helvetica Bold Underline.

TKSTEST Database

The TKSTEST database is the primary TKS database and contains the data from the papers.

Citation data

citation

The citation building block of the whole system. Generates a citation number which serves as the primary connector for all other tables. This holds either journal article or book chapter data.

citnumb - char(25) not null

The relation between all tables. The number will have the following format:

JBJB-JB-VVVV-PPPP-YYYY where:

JBJB = journal or book code (journalst.jcode or booklst.bcode)

VVVV = journal volume number or book chapter number, padded with zeros

PPPP = first page number, padded with zeros

YYYY = year of publication

This number will be generated from data entered in the other columns in the citation table.

citfile - char(20) not null

A filing system number for the paper. Also used in author-oriented access to system. Format may be used for citnumb in the future. The format for this number is:

AAAA.V.P.YY where:

AAAA = first four letters of first author's lastname

V = volume number

P = first page number

YY = last two digits of year

Number is automatically generated by application.

citserial - serial not null

serial number for each citation entry

citsource - char(20)

Source of the citation; the corresponding journalst.jcode or booklst.bcode

cltvol - char(4)

The journal volume number or book chapter number, not padded with zeros

cltpage - char(11)

The inclusive page numbers "PPPP-PPPP", not padded with zeros

cltdate - char(4)

The year of publication

clttitle - char(250)

The actual title of the paper or chapter

cltlocate - char(5)

The location of the actual paper in filing systems within the group

entrydate - date

The date the paper was first entered into the system.

authors

Author data for paper or chapter

aucitnumb - char(25) not null

The link to citation.citnumb

aucitfile - char(20)

Link to citation.citfile

auserial - serial not null

author entry serial number

authname - char(50) not null

The name of the author formatted as follows: last name, space, initials. No punctuation is to be used.

authsig - smallint not null

Publication order for the authors names

keywords

This table is to permit searching for unabstracted citations entered into the system. These will also be used to select citations for abstracting.

keycitrnumb - char(25) not null

The link to citation.citrnumb

keycitfile - char(20)

Link to citation.citfile

keyserial - serial not null

keyword serial number

keyword - char(20) not null

the keyword describing some aspect of the paper, matches the **keylist.kword**

keycode - char(10)

the keycode which can be used for group look-ups and is used to automatically insert the keyword when the code is entered. This is linked to the controlled vocabulary **keylist.kcode**

Materials and Methods data

paperover

The purpose for this table is to hold certain basic information about the paper. It holds the number of study designs within the paper as well as the purpose for the paper.

papcitrnumb - char(25) not null

The link to citation.citrnumb

papcitfile - char(20)

Link to citation.citfile

papserial - serial not null

paper overview serial number

papstatepur - char(50)

The stated purpose of the paper. This is both an evaluation point and information necessary to classify the paper.

papimppur - char(50)

The implied purpose of the paper. This can give insight into biases as well as "the real reason" for the study.

papaim - char(3)

A broad term to describe the aim of the study. This needs further clarification. Will be used to control analytical versus clinical studies paths for data entry.

papnumdsgn - smallint

The number of designs in the paper

studydsgn

The purpose for this table is to hold certain basic information about the study. It holds confirming information on the number of groups involved, the number of exposures involved, and the presence or absence of controls. There is a functional limit of 99 designs per paper.

stycitrnumb - char(25) not null

The link to citation.citrnumb

stycitfile - char(20)

The link to citation.citfile

styserial - serial not null

study design serial number; linked to sgdsgrnum, exdsgrnum, egdsgr

stydsgrncur - smallint

A number to identify this design from others in the paper. Used to link to subjgrp, exporegm, and expogrp.

stydsgrntot - smallint

The total number of study designs in the paper. Linked to paperover.papnumdsgr.

stytype - char(2)

The broad type of study. This is potentially useful in controlling the abstracting process.

styvivvit - char(2)

Indication of whether the paper describes an *in vivo* or an *in vitro* experiment.

stycntl - char(1)

Flag to whether controls were used or not.

stycnticmp - char(2)

The group comparison information. (Within group, between groups, combination)

stycmpmeth - char(2)

The method for comparing the groups regardless of within or between

stycntlmeth - char(2)

Control methodology base — concurrent vs non-concurrent

stycntltyp - char(2)

The type of control used for the respective method

stycntassgn - char(2)

the method for assigning the subjects to the group

stynumgrp - smallint

This is the number of different groups studied

stynumexp - smallint

The number of different exposure regimens used

subjgrp

This table holds data about each group of subjects in the study. Each group is now assigned a number. Formerly a letter from "A" to "Z" was assigned sequentially but this caused a number of problems. There is now a functional limit of 99 groups per study design.

sgcitnumb - char(25) not null

The link to citation.citnumb

sgserial - serial not null

subject group serial number

sgdsgrnum - integer

The link to the identifying serial number of the study design, ie. stdydsgr.styserial.

sglink - smallint

Used to in association with the stdydsgr.stydsgrncur and exporegm.exlink to form expogrp.eglink

sgspecies - char(20)

the species of the subjects used; not necessarily the Latin name. I would prefer to use English words instead.

sgbreed - char(20)

The breed, race, ethnic, or other genetic variation

sgsource - char(20)

source of subjects used in study

sgnumb - smallint

number of subject in group

sgage - char(4)

The age of the subjects. This will need to work with multiple subjects as well. Can average be used? Should this and the units be incorporated into one column and an agerange column be added?

sgageunit - char(1)

The units for the age of the subjects. This will need to work with multiple subjects as well. Can average be used? Should this and the weight be incorporated into one column and an agerange column be added?

sgagerange - char(1)

Groupings of ages into 5 categories

sgwt - smallfloat

The weight of the subjects. This will need to work with multiple subjects as well. Can average be used? Should this and the units be incorporated into one column and a weightrange column be added?

sgwtunit - char(2)

The units for the weight of the subjects. This will need to work with multiple subjects as well. Can average be used? Should this and the weight be incorporated into one column and a weightrange column be added?

sgwtrange - char(2)

Uses groupings of weight to allow sorting of animal weight data

sqht - char(4)

The height of the subjects. This likely to be only useful in human studies when it will allow determination of surface area. This will need to work with multiple subjects as well. Can average be used? Should this and the units be incorporated into one column and a heightrange column be added? Should this be deleted along with its units?

sghtunit - char(4)

The units for the height of the subjects. This will need to work with multiple subjects as well. Can average be used? Should this and the weight be incorporated into one column and a heightrange column be added?

sgsex - char(4)

The sex of the subject. This must cover multiple subjects, different sexes, and neutered animals.

sgoccup - char(20)

The occupation of the subjects; obviously aimed at human subjects.

sglthstat - char(20)

The health status of the subjects. Can include vaccinations, preexisting illnesses, etc.

sgtotexpo - smallint

The number of exposures this group received during the study.

exporegm

This table holds data about the exposure regimens that the subjects will undergo. Each regimen will be assigned a number between "00" and "99" and will be joined with the subject group number to create an exposure-group link.

excitnumb - char(25) not null

The link to citation.citnumb

exserial - serial not null

exposure regimen serial number

exdsignnum - integer

The link to the identifying serial number of the study design, ie. stdydsign.styserial.

exlink - smallint

The link to expogrp.eglink, numbers "00" to "99". Need to work out mechanism to handle treatment as well.

expurpose - char(3)

The purpose of the exposure. For example, toxicity or treatment.

exagent - char(40)

Agent in exposure regimen

exdose - char(5)

Dose of agent used (no units)

exdoseunit - char(6)

Units of dose administered

exformul - char(2)

Formulation of the agent used in the regimen. An abbreviation of the formulation will be used and an acceptable list of abbreviations will be maintained.

exroute - char(2)

Route of administering the agent in question. An abbreviation of the routes will be used and a list of acceptable abbreviations will be maintained.

exinterval - char(6)

The interval between multiple exposures, eg. every 4 hours. This will need some mechanism to handle erratic exposures.

exduration - char(10)

The duration of exposure to include both duration of contact as well as number of doses received.

exadminmeth - char(20)

The method of administering the agent to the subjects. Not to be confused with route. Example: slow IV via pump. IV is the route, the rest part of administration method.

exevaltime - char(20)

The time for evaluation; can be interval of evaluation if needed. This particular item may be better maintained in another table, such as study design..

expogrp

This table holds the links and brief description of the group and exposure regimen. This will be used to link results to the subjects and regimens.

egcitnumb - char(25) not null

The link to citation.citnumb

egserial - serial not null

exposure group serial number

egtotnum - smallint

The total number of exposure group links that have been made for this design. *Is this column really needed?*

eglink - char(11)

This will be used to link the subject group and exposure regimen of a study design to a given result. The format of this number is:

Dd.ss.Ee where:

- d = the current design number (stdydsgrn.stydsgrncur)
- s = the current subject group number (subjgrp.sglink)
- e = the current exposure regimen number (exporegmn.exlink)

This will be used as the value of clinfind.cfeglabel

egdsgn - integer

Direct link to stdydsgrn.styserial.

egdsgnlabel - smallint

The value of stdydsgrn.stydsgrncur; used to create the eglink.

egdsgndsc - char(60)

Brief description of the study design. This is used to confirm on screen the design data when associated result data is entered. This should be generated by the computer and inserted when the user selects the study design data.

egsubg - integer

Direct link to subjgrp.egserial.

egsublabel — smallint

The value of subgrp.sglink; used to create the eglink.

egsubgdsc — char(60)

Brief description of the subject group. This is used to confirm on screen the group data when associated result data is entered. This should be generated by the computer and inserted when the user selects the exposure regimen data.

egexpo — integer

Direct link to exporegm.exserial.

egexpolabel — smallint

The value of exporegm.exlink; used to create the eglink.

egexpodsc — char(60)

Brief description of the exposure regimen. This is used to confirm on screen the exposure data when associated result data is entered. This should be generated by the computer and inserted when the user selects the exposure regimen data.

Results data

The results tables need to manage repeated values, lab data, and be more easily accessed.

clinfind

cfcltnumb — char(25) not null

The link to citation.citnumb

cfserial — serial not null

serial number for clinical findings

cfeglink — integer

This links to expogrp.egserial

cfeglabel — char(11)

This links to expogrp.eglink

cfstype — char(1)

Whether the finding is a lab test, morphologic change, or sign/symptom/disease. Used to direct abstracting flow.

cfstecode — char(6)

Link to tkssite.sitecode which will in turn is linked to the associated site of the clinical finding.

cfsite — char(70)

The anatomical site of the clinical finding. Linked to the tkssite.locatename via the tkssite.sitecode.

cffindcode — char(8)

Link to tkssite.findcode which will in turn is linked to the associated the clinical finding.

cffinding — char(70)

The clinical finding from the tkssite.findterm.

cfchange — char(10)

The type of change which occurred. Uses the SNOMED functional change codes to insert the appropriate terms in this column. This needs to be reduced to a single digit code and use translation functions to generate.

cfsevvalue — char(8)

The severity of the clinical finding. Estimated severity in non-lab values (1+ to 3+). For lab values, this is the specific lab finding.

cfsevunits — char(8)

The units used in the lab value from cfsevvalue.

cffreq — char(6)

The frequency of the finding in the group. Must resolve whether this should hold both numerator and denominator or just the numerator.

cfonset - char(10)

The time to onset in hours from the time of exposure.

cfduration - char(10)

The duration of the clinical finding from time of onset to termination of the observation.

Discussion data

Reference data

Evaluation data

tkacomment

cocitnumb - char(25) not null

The link to citation.citnumb

cocitfile — char(20)

Link to citation.citfile

coserial - serial not null

comment serial number

cotabname — char(20)

The name of the table holding the data being commented on.

cocolname — char(20)

The name of the column holding the data being commented on.

corownumb — integer

The row number of the row holding the data being commented on.

cotext - char(300)

Comments that the abstractor made about the paper. Could also be used for comments from the discussion section of the paper being reviewed. May be comments made by one author about the contents of another paper.

corefcrfile — char(20)

The source of the comment:

the TKS abstractor

link to the author of this paper

link to the author of another paper

Vocabulary Data

Journalst

The purpose of this table is to provide a controlled listing of journals to be used in the citation process. This will permit journals and book citations to be entered in a similar fashion with the unique aspects of each maintained in their respective tables.

jaquis - serial

Serially assigned number for each journal in the system

jcode - char(20)

A unique code for each journal in system composed of "J" and the jacquis number. While this number is 20 characters long in the database table, only 6 characters are actually used. The 20 characters are necessary to join the serial table and and the "J" together.

jname - char(120)

The exact name of the journal. Most are taken from the List of Journals Indexed by NLM.

jabrv - char(50)

Journal abbreviation, generally taken from List of Journals Indexed by NLM. These will be used in the reference listings and to display on screen when a journal code is entered in the citation table.

booklist

The purpose of this table is to provide a controlled listing of books to be used in the citation process. This will permit journals and book citations to be entered in a similar fashion with the unique aspects of each maintained in their respective tables.

bacquis - serial

Serially assigned number for each book in the system

bcode - char(20)

A unique code for each book in system composed of "B" and the **bacquis** number. While this number is 20 characters long in the database table, only 6 characters are actually used. The 20 characters are necessary to join the serial table and the "B" together.

bname - char(60)

The actual title of the book

bedno - char(2)

The edition number of the book

bvol - char(2)

The volume number of the book

bdate - char(4)

The year of the book's publication: should be edition specific.

bpub - char(20)

Publisher of this edition of the book

bpubplace - char(20)

Place of publication of this edition

beditor - char(50)

The editors of this edition of the book or the author(s) if not an edited work. This is a simple string and is not intended to do any more than complete the citation in a bibliography, etc.

bisbn - char(20)

This is the ISBN number for the book. This very well may be dropped in the future.

keylist

The purpose of this table is to provide a controlled vocabulary for keyword entry into the system.

kcode - char(10)

Code number for linking the keyword. User can enter a **kcode** and the **kword** will pop up on screen. This can also be used to query for a group of keywords of the same group.

kword - char(20)

The controlled keyword vocabulary. These are arranged by group.

tkssite

This file holds the basic topography information for showing the site of the clinical finding. Modified information from SNOMED/SNOVET with our enhancements.

sitecode — char(6)

Code used to link the anatomic site to the clinical finding. Composed of a system code (A to Z) and a location code (digits 3 to 6 of SNOMED/SNOVET topography number)

systemcode — char(1)

Alphabetical value used in site code.

systemname — char(30)

Internal system name plus SNOMED/SNOVET system name when needed

organcode — char(2)

Code representing the organ or organ group. Uses the SNOMED two character code.

organname — char(60)

Name of the organ or organ group. Uses the SNOMED name.

locatecode — char(5)

Code representing the specific site of the lesion. This is usually a subdivision of the organ or organ group. Uses digits 3 to 5 of the SNOMED topographic code.

locatename — char(60)

The name of the specific organ or organ group site. Uses the SNOMED name. Many are too long and maybe too specific.

snotopnum — char(8)

The SNOMED/SNOVET coding number.

morphlst

The purpose of this table is to provide a smaller, more manageable, controlled vocabulary for morphologic findings. This table consists primarily of SNOMED/SNOVET morphology findings.

morphnum char(6)

Code number linked to *morphsynlst.morphcode*

morphterm char(60)

The TKS controlled vocabulary term for morphologic finding.

morphdef char(65)

The TKS definition for the morphologic finding

morphsnocde char(8)

The SNOMED/SNOVET code number for the term in the SNOMEDVET database.

morphsnotrm char(65)

The SNOMED/SNOVET term in the SNOMEDVET database.

morphsynlst

morphcode char(6)

Code number linked to *morphlst.morphnum*

morphsyn char(60)

Synonym for the corresponding *morphlst.morphterm*

lablst

labnum char(6)

Code number linked to *labsynlst.labcode*

labterm char(60)

The TKS controlled vocabulary term for the laboratory test/finding or procedure.

labdef char(65)

The TKS definition of the controlled vocabulary term for the laboratory test/finding or procedure.

labsnocde char(8)

The SNOMED/SNOVET code number for the term in the SNOMEDVET database.

labenotrm char(65)

The SNOMED/SNOVET term in the SNOMEDVET database.

labsynlst

labcode char(6)

Code number linked to *lablst.labnum*

labsynsys char(1)

Code letter for the laboratory grouping

labsyn char(60)

Synonyms for the corresponding *lablst.labterm*

signlst

signnum char(6)

Code number linked to **signsynlst.signcode**

sign char(60)

The TKS controlled vocabulary term for the disease, clinical finding, sign, or syndrome.

systemcode char(1)

The TKS code for the body system primarily involved. Related to **tkssite.systemcode**.

systemname char(30)

The TKS name for the body system primarily involved. Related to **tkssite.systemname**.

signdef char(65)

The TKS definition of the controlled vocabulary term for the disease, clinical finding, sign, or syndrome.

snocode char(8)

The SNOMED/SNOVET code number for the term in the SNOMEDVET database.

snoterm char(65)

The SNOMED/SNOVET term in the SNOMEDVET database.

signsynlst

signcode char(6)

Code number linked to **signlst.signnum**

signsynsys char(1)

The code for the body system

signsyn char(60)

Synonyms for the corresponding **signlst.signterm**

SNOMEDVET Database

The SNOMEDVET database contains the compiled SNOMED and SNOVET terms in a relational database form. This database was used to extract needed clinical finding vocabulary terms for the TKSTEST database.

Topography

snotopograph

topognum - char(8)

topogterm - char(100)

Functions

snofunction

functnum - char(8)

functterm - char(100)

Diseases

snodisease

diseasenum - char(8)

diseaseterm - char(100)

Procedures

snoproced

procednum - char(8)

procedterm - char(100)

Appendix C.
Keywords Available for Use in
Toxin Knowledge System

Mycotoxins	
A01	OCHRATOXIN
A02	HT-2
A03	T-2
A04	AFLATOXIN
A05	T-2 TRIOL
A06	DAS
A07	OTH NONTRICHS
A08	T-2 TETRAOL
A09	DON
A10	MULTI MYCO
A11	3-ACETYL DON
A12	NIV
A13	MAS
A14	NEOSOLANIOL
A15	ZEN
A16	DEEPOXY
A17	FUSARENON
A18	MACRO
A19	VERRUCARIN A
A20	CYANIDE
A21	ZOL
A23	ACETYL T-2
A24	OTH TRICHS
A25	RORIDIN

Military Issue	
B01	YELLOW RAIN
B02	CHEM WAR

Species	
C01	BOV DAIRY
C02	RAT
C03	MOUSE
C04	BOV BEEF
C05	SWINE
C06	SHEEP
C07	BOV
C08	HUMAN
C09	MONKEY
C10	DOG
C11	HORSE
C12	CAT
C13	HAMSTER
C14	RABBIT
C15	FISH
C16	G PIG
C17	CHICKEN
C18	TURKEY
C19	DUCK
C20	PIGEON
C21	OTHER SPECIES

Gender	
D01	MALE
D02	FEMALE
D03	NEUTERED

Age		Chemical Techniques	
E01	FETUS	I01	DERIV
E02	NEONATE	I02	HFB
E03	YOUNG	I03	TMS
E04	MIDAGE	I04	TFA
E05	AGED	I05	PFP
E06	EGG		
E07	LARVAE		
Sources/Form		Extractants	
F01	MOLDY FEED	J01	ACETONE
F02	FUNGUS	J02	WATER
F03	CRUDE EXTRACTS	J03	SALINE
F04	CRYSTAL	J04	CHLOROFORM
F05	AEROSOL	J05	CAR ETHANOL
		J06	ETHYL ACET
		J07	PROP GLY
		J08	CAR NONE
		J09	METHANOL
		J10	CAR DMSO
		J11	CAR OTHER
Toxicity Results		Sample Matrix	
G01	LO	K01	SAMPLE MATRIX
G02	LD50	K02	FEED
G03	>LD50<LD100	K03	FOOD
G04	>LD100	K04	PRODUCTION
G05	LD100	K05	URINE
G06	LC50	K06	BLOOD
Route of Administration		K07	MILK
H01	IM	K08	BILE
H02	IV	K09	FECES
H03	IP	K10	RUMEN CONT
H04	ORAL GAVAGE	K11	SERUM
H05	TOPICAL	K12	GRAIN
H06	ORAL DIET	K13	FORAGES
H07	SUB Q	K14	CEREAL
H08	INTRATRACH	K15	STRAW
H09	INTRADER	K16	CORN
H10	GASTRIC INTUBATION	K17	OATS
H11	MULTI DOSE	K18	BARLEY
H12	INHAL		

K19 MILLET
 K20 SOYBEAN
 K21 HULLS
 K22 RICE
 K23 WHEAT
 K24 SORGHUM
 K25 MEDIA
 K26 FUNGAL
 K27 PLASMA
 K28 OTHER MATRIX

Chemical Info

L01 TOXIN CHAR
 L02 STRUCT ID
 L03 SYNTHESIS
 L04 DEGRAD
 L05 DETOX

Analytical

M01 ANAL
 M02 ANAL GLC
 M03 BIOAS
 M04 NMR
 M05 RIA
 M06 ANAL ENZ
 M07 PURIFIC
 M08 TLC
 M09 MS
 M10 HPLC
 M11 GS/MS
 M12 AUTORAD
 M13 FLUOR
 M14 RADIOLABEL
 M15 CAP GC
 M16 TISS CULT
 M17 SPECTRO
 M18 CELL-FREE SYS

Mechanism of Action

N01 MECH ACTION
 N02 PROT SYN
 N03 DNA SYN
 N04 ENERG MET
 N05 MEMB EFFEC
 N06 ENZ INHIB
 N07 ANTI MITOT
 N08 CHELATE
 N09 OTHER MECH

Toxicokinetics

O01 ABSORB
 O02 DISTRI
 O03 EXCRE
 O04 BOD BURD
 O05 TISS RESID
 O06 BOD FLU RESID

Metabolism

P01 METAB
 P02 METAB IN VITRO
 P03 METAB IN VIVO
 P04 DEEPOXY METABS
 P05 CONJU METABS

Toxicity Info

Q01 TOX
 Q02 TOX IN VITRO
 Q03 TOX IN VIVO
 Q04 REPRO
 Q05 PLACENTA
 Q06 UTERUS
 Q07 FETUS-TOX
 Q08 TESTES
 Q09 OVARIES
 Q10 TERATO
 Q11 CARCIN
 Q12 GUT FLORA
 Q13 ABORT

Q14 MUTAG
 Q15 SURV RATE
 Q16 SURV TIME
 Q17 GROWTH
 Q18 FEED REFUS
 Q19 FEED EFFIC
 Q20 FEED CONSUMP
 Q21 ACUTE
 Q22 CHRONIC
 Q23 WATER CONSUMP

Clinical Findings

R01 PHYSIOLOGY
 R02 CLIN SIGNS
 R03 SHOCK
 R04 COLD EXTREM
 R05 BLOOD FLOW
 R06 DIARRHEA
 R07 HEMMOR
 R08 VOMITING
 R09 POST ATAX/WEAK
 R10 IN CRT
 R11 BLOOD PH
 R12 IMMUNE
 R13 BLOOD GAS
 R14 CNS
 R15 PNS
 R16 GASTRIC PH
 R17 LUNG
 R18 BRAIN
 R19 CHILLS
 R20 FEVER
 R21 GI
 R22 GI PERISTALSIS
 R23 BLOOD PHYSIOLOGY
 R24 CVP
 R25 HEART
 R26 EKG

R27 KID FUNC
 R28 PROSTAGL
 R29 EDEMA
 R30 RESP FUNC
 R31 BLOOD PRES
 R32 CLOTING
 R33 LIV FUNC
 R34 CARDIAC OUTPUT
 R35 DEATH
 R36 HEART RATE
 R37 PREGNANT
 R38 TREMORS

Gross Pathology

S01 GROSS
 S02 PATH HISTO
 S03 PATH BODY
 S04 CLIN SIGNS PATHOLOGY
 S05 PATH ORAL
 S06 PKID
 S07 PRES P TRAC
 S08 PPAN
 S09 PDIG TRAC
 S10 PSKIN
 S11 PVESS
 S12 PHEART
 S13 PLIV
 S14 PBONE MARROW
 S15 PSPLEEN
 S16 PADRENAL
 S17 PNER SYS
 S18 PLYMPH
 S19 PREPRO MALE
 S20 PTHYMUS
 S21 SEM
 S22 TEM
 S23 PREPRO FEMALE
 S24 PATH CLIN

S25 PLATELETS
 S26 PPLACEN
 S27 CBC
 S28 PCV-PVC
 S29 WBC
 S30 RBC
 S31 CLOT
 S32 CLIN SER ENZ
 S33 CLIN ENZ

U10 PESTICIDES
 U11 MODEL
 U12 IN VIVO
 U13 INSECTICIDES
 U14 PHARM
 U15 ADSORPTIVE CAPACITY
 U16 COMBINATIONS
 U17 RISK ASSESSMENT
 U18 PRODUCTION REVIEW

Therapy

T01 THERAPY
 T02 CHARCOAL
 T03 DRUG
 T04 ANTIBI
 T05 FLUIDS
 T06 ANTI BOD
 T07 VIT C
 T08 VIT K
 T09 STEROIDS
 T10 EFFEC
 T11 NONEFFEC
 T12 THIOCYANATE
 T13 OTHER THERAPY

Study Type

U01 REVIEW
 U02 SURVEY
 U03 DIAG
 U04 TECHNIQUES
 U05 NAT OCCUR
 U06 STATISTICS
 U07 SYNERGISM
 U08 LIGNANS
 U09 IN VITRO

Appendix D.
Graphical Depiction
of
Toxin Knowledge System
Application Menu Structure

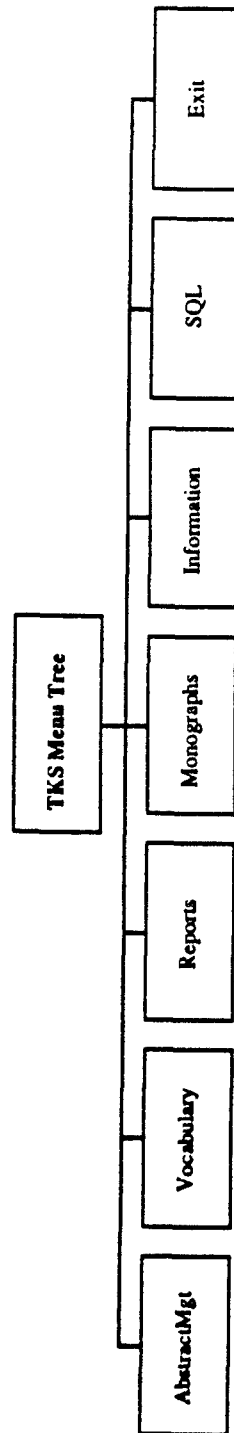


Figure 26. Main Menu of Toxin Knowledge System Application

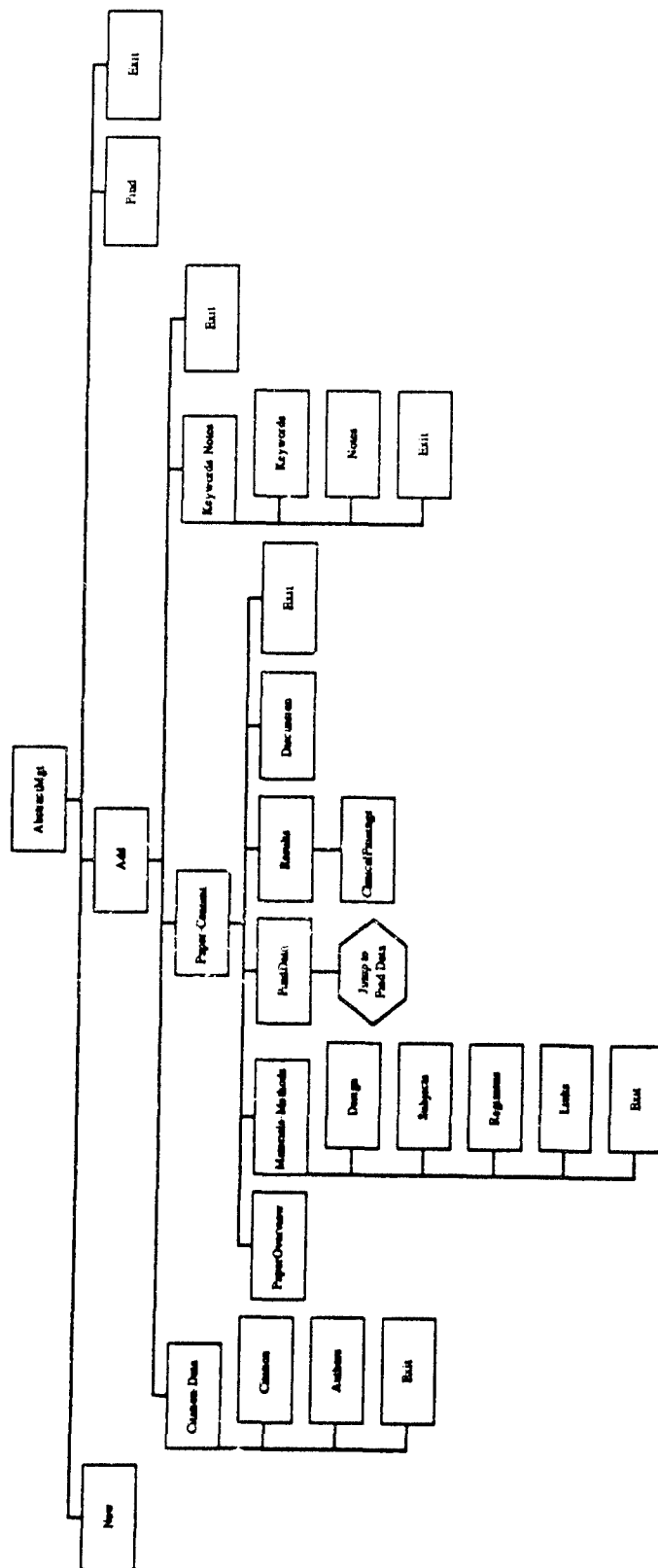


Figure 27. New and Add Submenus of the AbstractMgt Choice from the Main Menu

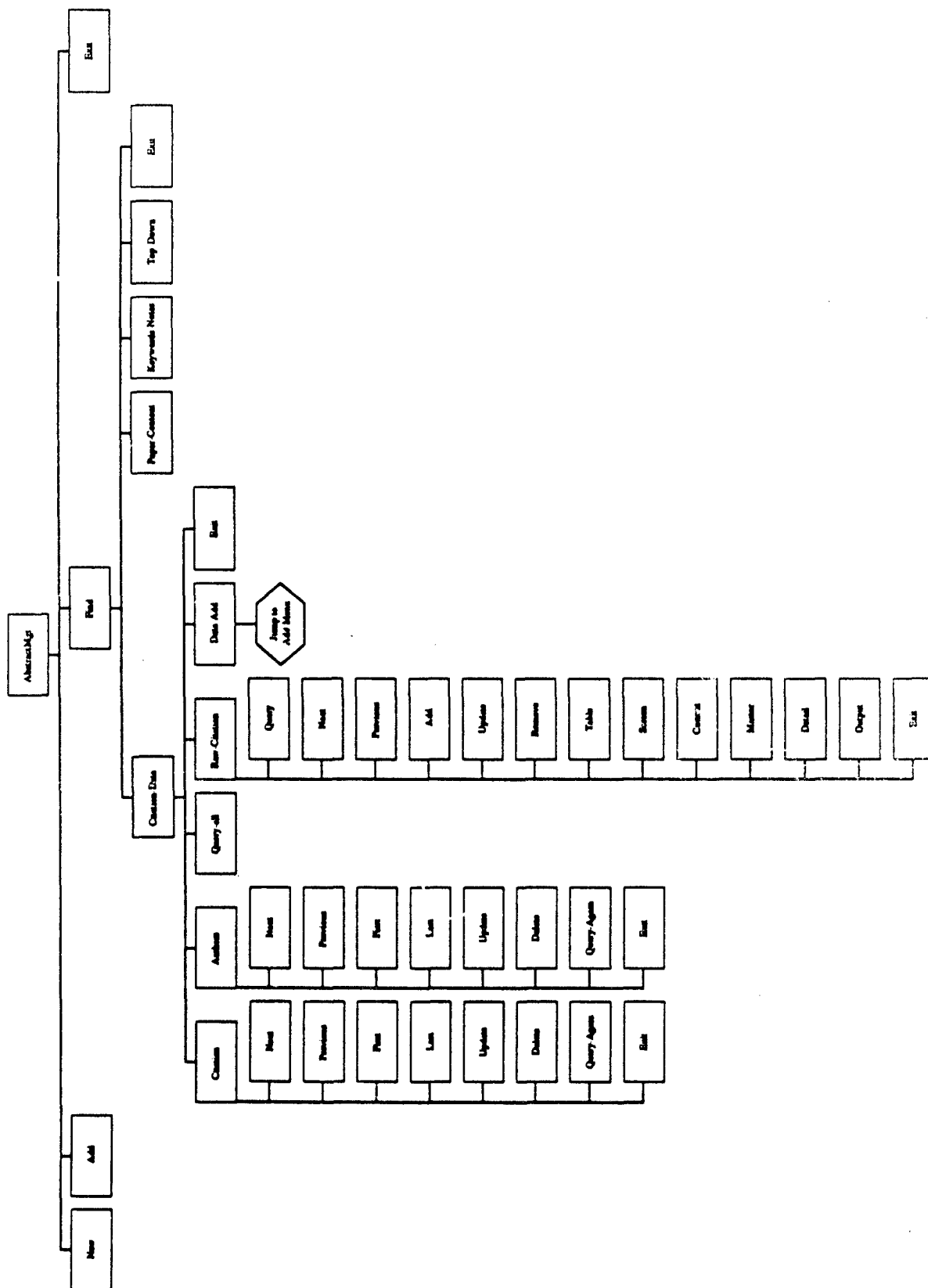


Figure 28. Find Citation Data Submenus of the AbstractMgt Choice from the Main Menu

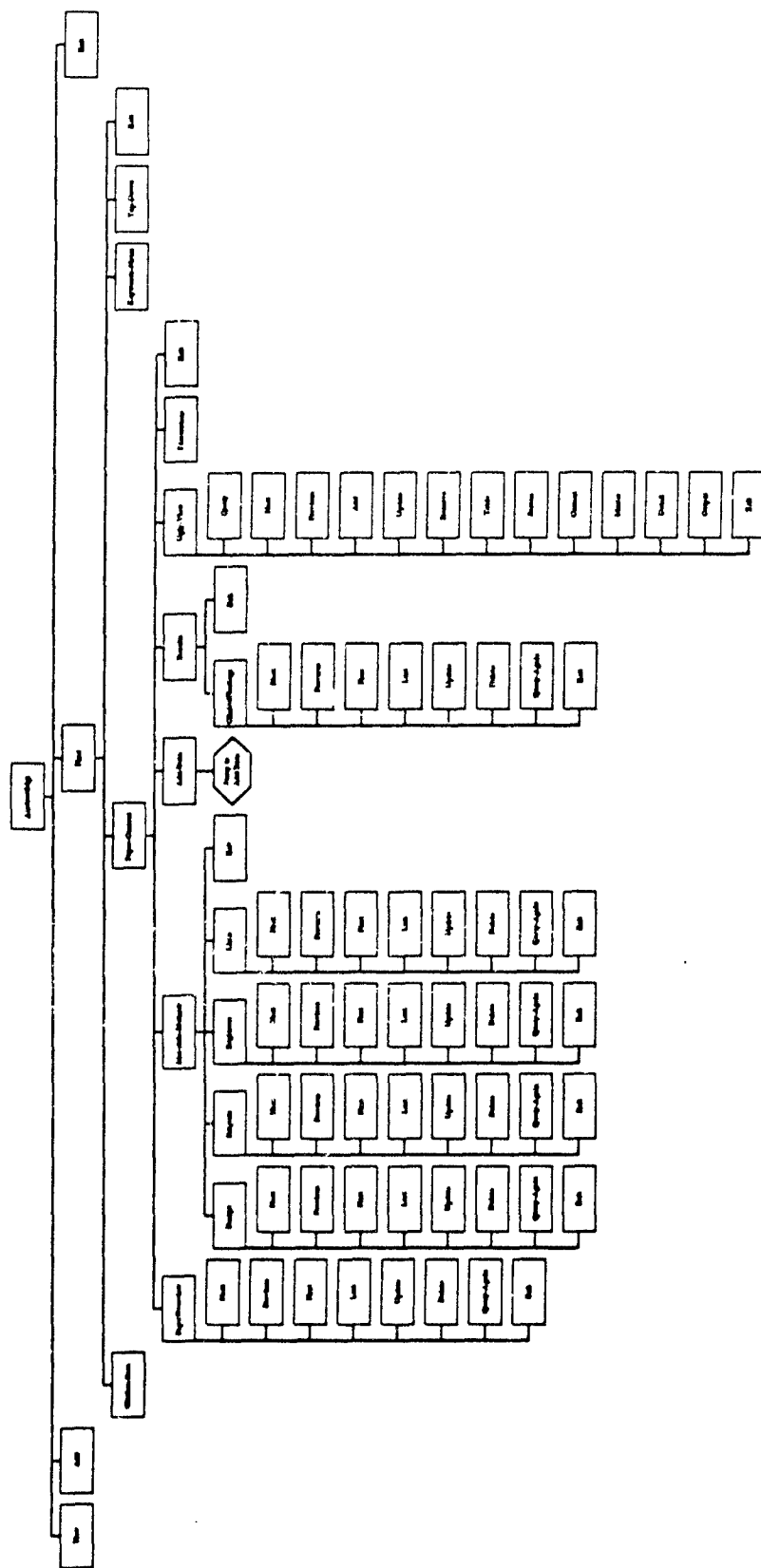


Figure 29. Find Paper-Content Submenus of the AbstractMgt Choice from the Main Menu

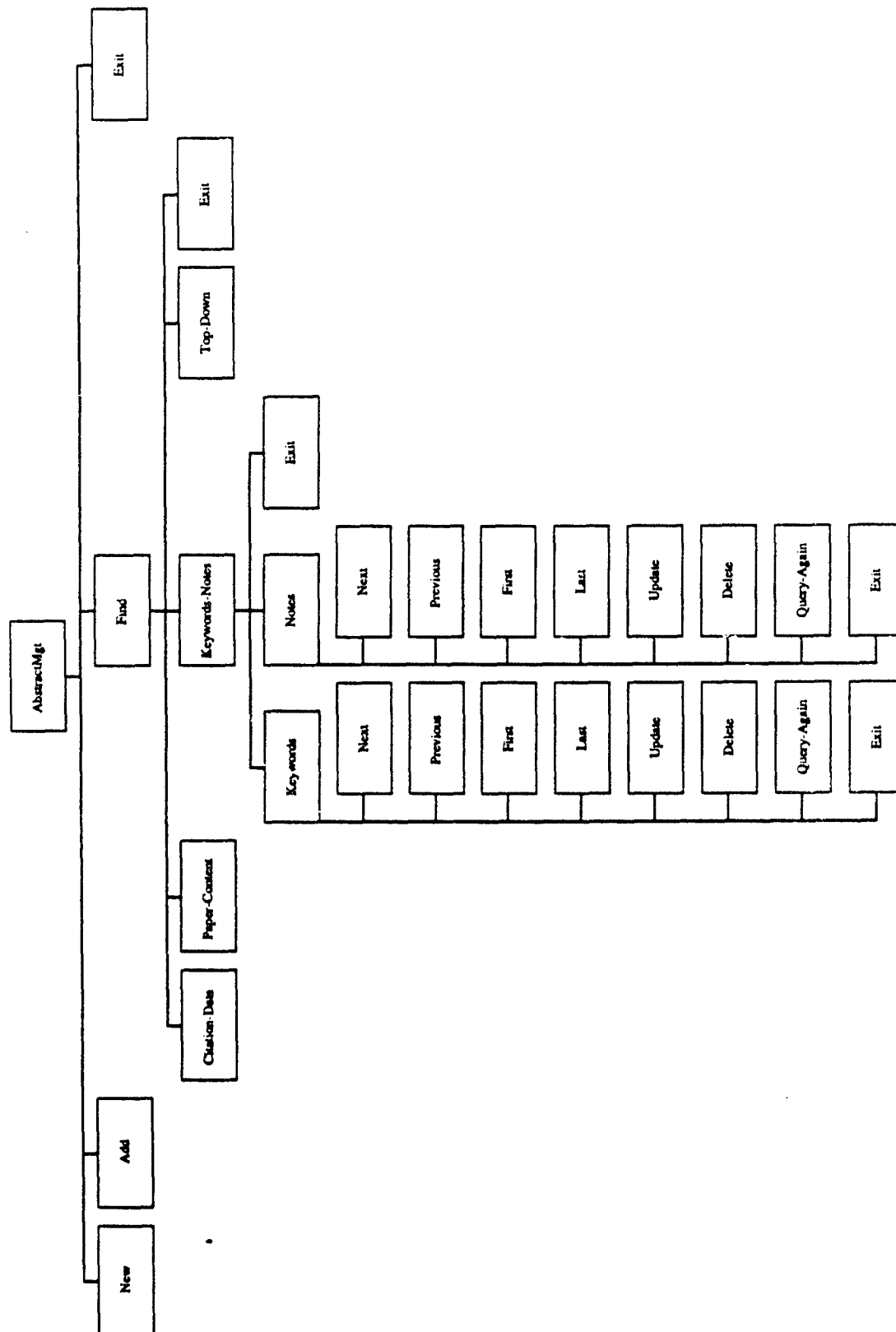


Figure 30. Find Keywords-Notes Submenus of the AbstractMgt Choice from the Main Menu

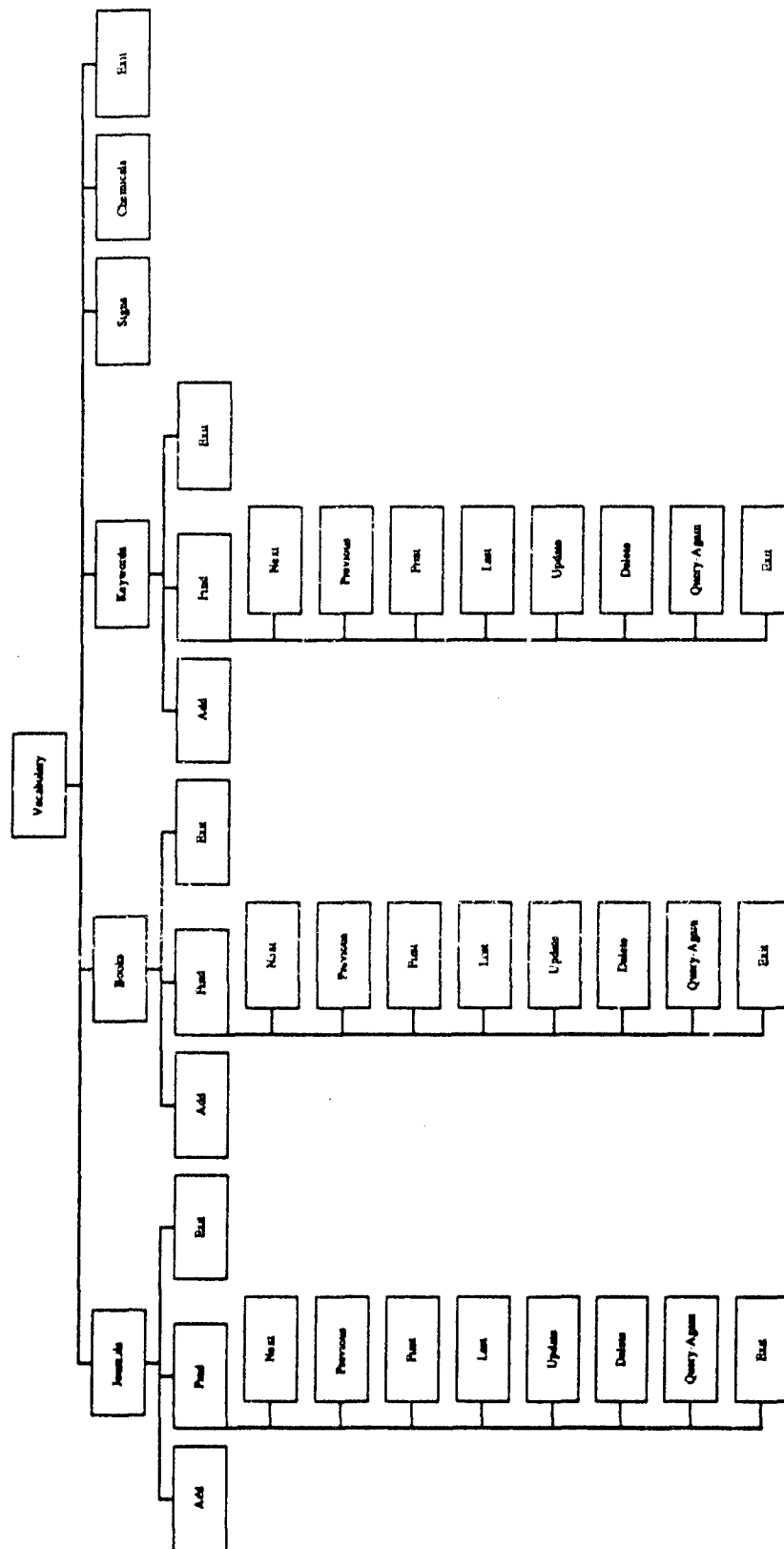


Figure 31. Journals, Books, and Keywords Submenus of the Vocabulary Choice from the Main Menu

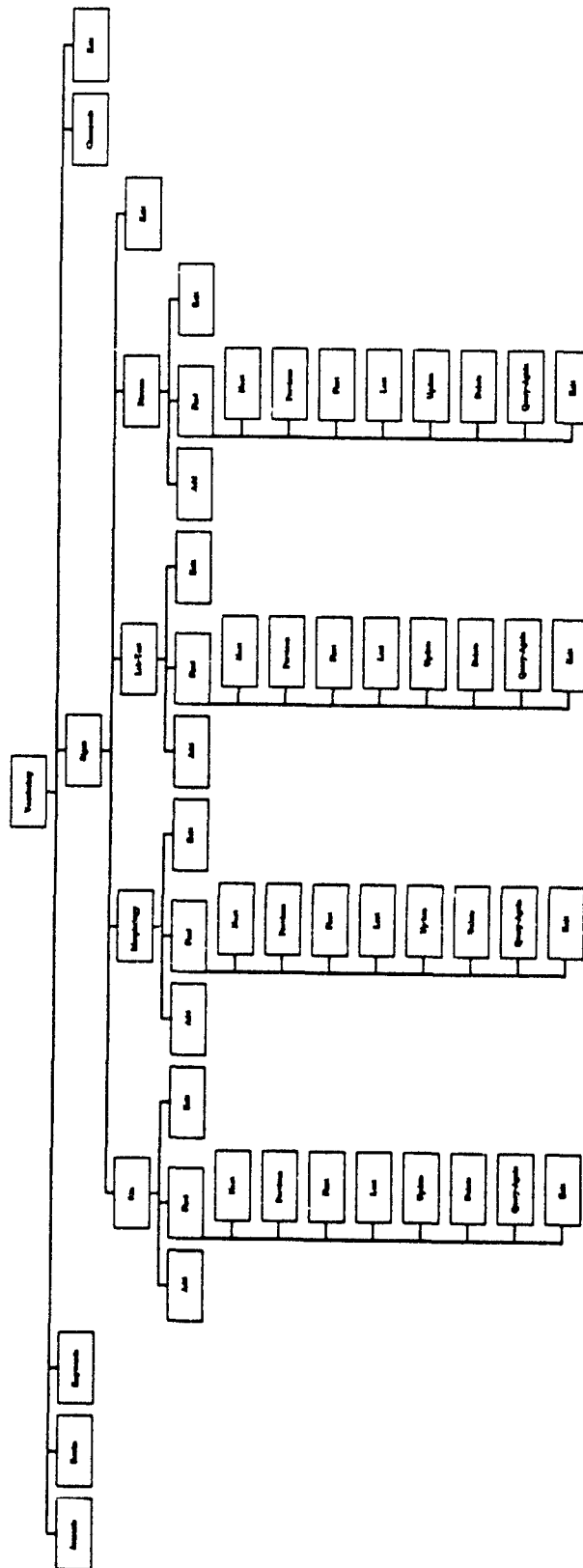


Figure 32. Signs Submenus of the Vocabulary Choice from the Main Menu

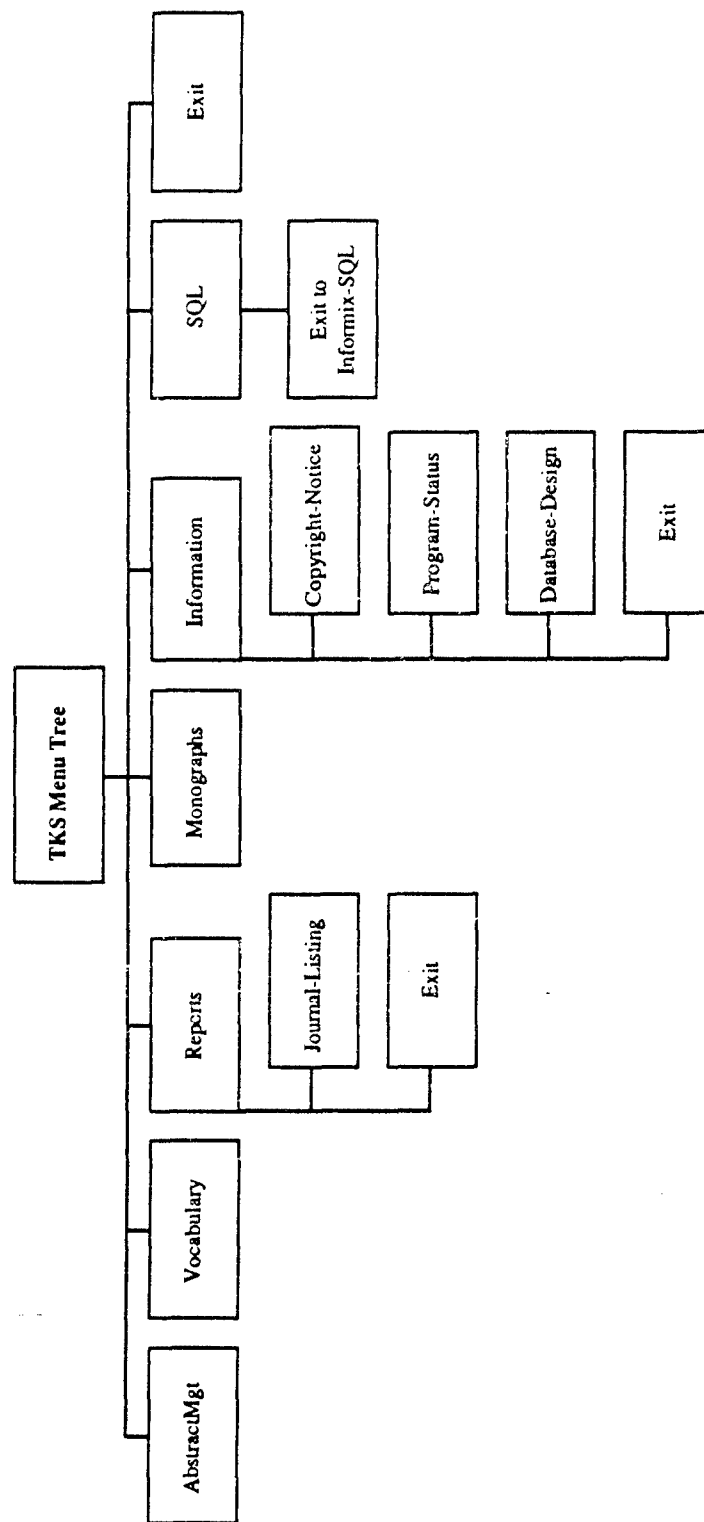


Figure 33.Submenus for the Reports, Information, and SQL Choices from the Main Menu

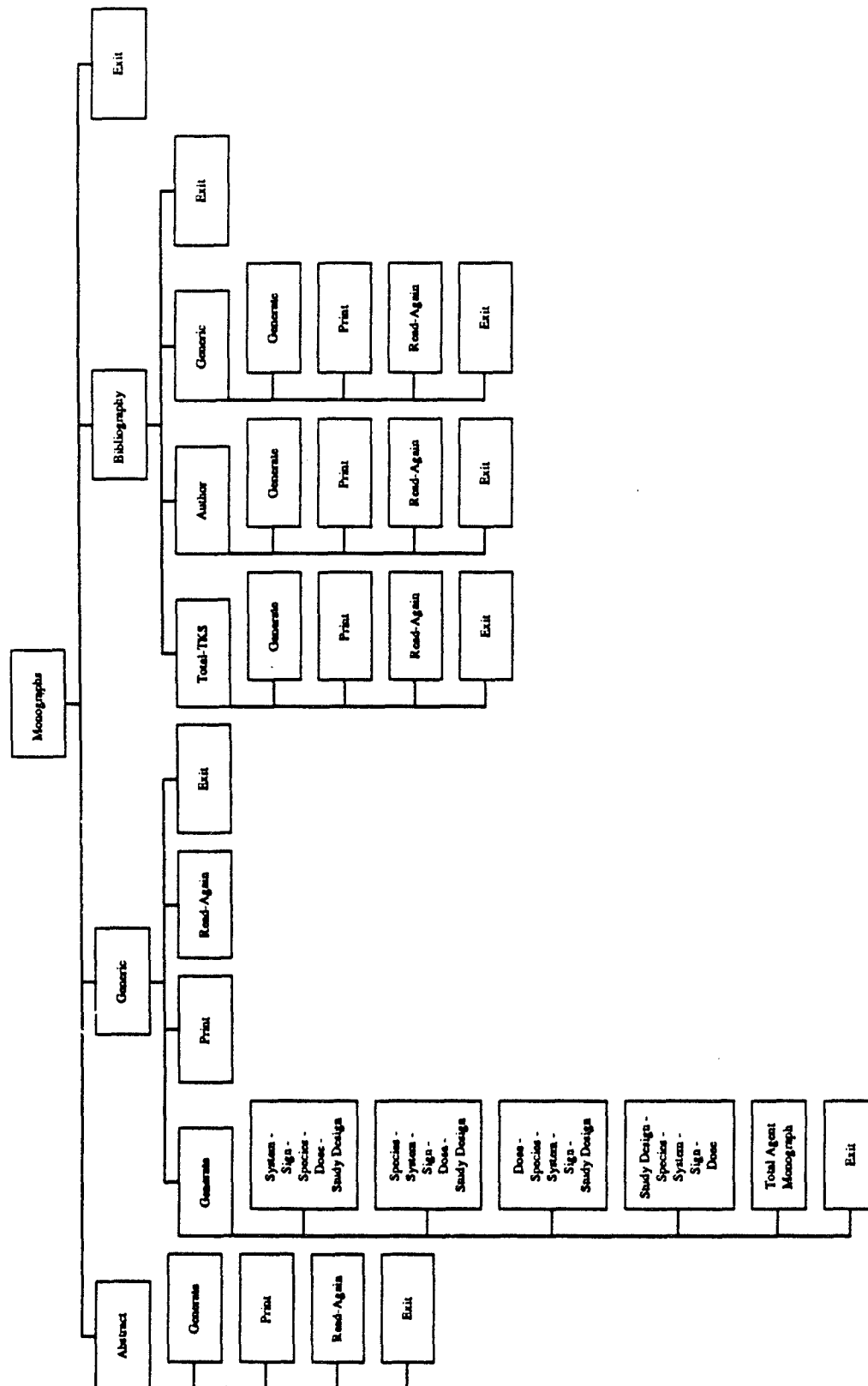


Figure 34. Submenus for the Monographs Choice from the Main Menu

Appendix E.
Citations Entered into
Toxin Knowledge System

- (945) Aas P, Sterri SH, Hjermstad HP, Fonnum F: A METHOD FOR GENERATING TOXIC VAPORS OF SOMAN: TOXICITY OF SOMAN BY INHALATION IN RATS, *TOXICOL APPL PHARMACOL* 80:437-445, 1985
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- (943) Abou-Donia MB, Lapadula DM, Cambell G, Timmons PR: THE SYNERGISM OF N-HEXANE-INDUCED NEUROTOXICITY BY METHYL ISOBUTYL KETONE FOLLOWING SUBCHRONIC (90 DAYS) INHALATION IN HENS: INDUCTION OF HEPATIC MICROSOMAL CYTOCHROME P450, *TOXICOL APPL PHARMACOL* 81:1-16, 1985
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- (362) Achilladelis B, Hanson JR: MINOR TERPENOIDES OF *TRICOTHECIUM ROSEUM*, *PHYTOCHEM* 8:765-767, 1969
- (2842) Ackerman S: LAST WORD ON YELLOW RAIN?, *SCIENCE* 115:32-32, 1987
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- (2163) Adelman WJ, Fohlmeister JF, Sasner JJ JR., Ikawa M: SODIUM CHANNELS BLOCKED BY APHANTOXIN OBTAINED FROM THE BLUE-GREEN ALGA, *APHANIZOMENON FLOSAQUAE*, *TOXICON* 20:513-5516, 1982
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- DEGRADATION IN THE CYANOBACTERIUM APHANOCAPSA 6308, J BACTERIOL 141:687-693, 1980
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**Appendix F.
Sample Monographs
Generated by the
Toxin Knowledge System
Application**

Structured Abstracts

TKS Citation code: J00117-0178-00274-1981

File code: ANGS.178.274 81 in the following files: LP

(1883) Angsubhakorn S, Poomvises P, Romruen K, Newberne PM: AFLATOXICOSIS IN HORSES, J AM VET MED ASSOC 178:274-278,1981

Keywords Assigned: horse, aflatoxin, kid func, diag, feed, anal, corn, hemmor, death, clin signs, heart, fluids, rice, rbc, serum, soybean

ABSTRACT

Overview:

CASE REPORT paper with stated purpose of DOCUMENT AFLATOXIN POISONING IN HORSES reporting on 2 design(s).

Design Information:

Results: Design-Oriented

Design: 1 GRP, 1 EXP, CNTL

Subjects: 12 HORSE, Age: <1 Y, Wt: KG, Sex: M, EXP

Exposure Regimen: AFLATOXIN, 216 UG/KG, PO, given x FEW DAYS

UNK SEVERITY PETECHIA in HEART, NOS seen in NOT ST subjects

UNK SEVERITY MYOCARDIAL NECROSIS SYNDROME, NOS in MYOCARDIUM, NOS seen in NOT S subjects with onset of UNK hour(s)

UNK SEVERITY HEMORRHAGIC ENTERITIS (T-64000) in GASTROINTESTINAL TRACT, NOS seen in UNK subjects

UNK SEVERITY BILE STASIS in LIVER, NOS seen in NOT ST subjects

UNK SEVERITY INFILTRATION, FATTY in LIVER, NOS seen in UNK subjects

UNK SEVERITY INFLAMMATORY NECROSIS, NOS in LIVER, NOS seen in NOT ST subjects

UNK SEVERITY HYPERPLASIA, NOS in INTRAHEPATIC BILE DUCT seen in NOT ST subjects

UNK SEVERITY NECROSIS, NOS in CENTRIOBULAR REGION OF LIVER seen in NOT ST subjects with onset of NOT ST hour(s)

UNK SEVERITY FIBROSIS, NOS in PERIPHERAL LOBULAR REGION OF LIVER seen in NOT ST subjects

UNK SEVERITY EDEMA, NOS in KIDNEY, NOS seen in NOT ST subjects

UNK SEVERITY PALE RED COLOR in KIDNEY, NOS seen in UNK subjects

UNK SEVERITY DEATH, NOS in seen in 12/? subjects with onset of FEW DAYS hour(s)

Design: GRP, EXP, CNTL

No results reported for this Exposure Group.

Subjects: 2 HORSE, Age: UNK Y, Wt: KG, Sex: UNK, EXP

Exposure Regimen: PRESUMABLY NO AFLATO, , PO, given x UNK

No results reported for this Exposure Group.

TKS Citation code: J00005-0049-00482-1988

File code: HAK - 49 482.88 in the following files: P

(2556) Harvey RB, Muff WE, Kubena LF, Carrier DE, Phillips TD: PROGRESSION OF AFLATOXICOSIS IN GROWING BARROWS, AM J VET RES 49:482-487,1988

Keywords Assigned: aflatoxin, pliv, serum, pthymus, pbone marrow, prot syn, feed, g pig, pregnant, rat, feed effic, feed consump, don, zen, ochratoxin, gs/ms, sem, anal, swine, aged

ABSTRACT

Overview:

EXPER-TOXICITY paper with stated purpose of PATHOGENESIS OF AFLATOXICOSIS IN GROW. BARROWS and implied purpose of CLINICAL DIAGNOSIS OF AFLATOXICOSIS reporting on 1 design(s).

Design Information:

Results: Design-Oriented

Design: 5 GRP, 5 EXP, Y CNTL

Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP

Exposure Regimen: NONE, CLEAN FEED, 0 MG/KG, PO, given CHRON x 28 D
UNK SEVERITY NORMAL CONDITION in BODY AS A WHOLE seen in 5/5 subjects

Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP

Exposure Regimen: AFLATOXIN, 1 MG/KG, PO, given CHRON x 28 D
UNK SEVERITY NORMAL CONDITION in BODY AS A WHOLE seen in 5/5 subjects

Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP

Exposure Regimen: AFLATOXIN, 2 MG/KG, PO, given CHRON x 28 D
UNK SEVERITY NORMAL CONDITION in BODY AS A WHOLE seen in 5/5 subjects

Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP

Exposure Regimen: AFLATOXIN, 3 MG/KG, PO, given CHRON x 28 D
No results reported for this Exposure Group.

Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP

Exposure Regimen: AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D
UNK SEVERITY LIPIDOSIS, NOS in LIVER, NOS seen in 5/5 subjects

ASPARTATE AMINO TRANSFERASE (SGOT) MEASUREMENT (F-23160) (41 IU/L) in SERUM seen in MEAN subjects with onset of 14 DAYS hour(s) and duration of 14 DAYS hour(s).

CREATINE KINASE (CK) (109 IU/L) in SERUM seen in MEAN subjects with onset of 28 DAY hour(s)

GAMMA GLUTAMYL TRANSPEPTIDASE, SERUM, MEASUREMENT (GGT) (F-21340)

(29 IU/L) in SERUM seen in MEAN subjects with onset of 14 DAYS hour(s) and duration of 14 DAYS hour(s).

LACTIC DEHYDROGENASE ISOENZYME, NOS (277 IU/L) in SERUM seen in MEAN subjects with onset of 28 DAY hour(s)

UNK SEVERITY PHOSPHORUS, DECREASED LEVEL in SFRUM seen in MEAN subjects with onset of 21 DAYS hour(s) and duration of 7 DAYS hour(s).

UNK SEVERITY ICTERUS, NOS in SKIN, NOS seen in 2/5 subjects with onset of 25 DAYS hour(s)

UNK SEVERITY DRY STRUCTURE in HAIR, NOS seen in 5/5 subjects with onset of UNK hour(s) and duration of UNK hour(s).

UNK SEVERITY CACHEXIA in BODY AS A WHOLE seen in 5/5 subjects with onset of UNK hour(s) and duration of UNK hour(s).

TKS Citation code: J00001-0005-00879-1985

File code: BEAS.5.879.85 in the following files: S P

(1410) Beasley VR: EXPERIMENTAL T-2 TOXICOSIS IN SWINE I. CHANGES IN CARDIAC OUTPUT, AORTIC MEAN PRESSURE, CATECHOLAMINES, 6-KETO-PGF1ALPHA, THROMBANE B2, AND ACID-BASE PARAMETERS, FUNDAM APPL TOXICOL 5:879-892, 1985

Keywords Assigned: blood gas, blood ph, clin ser enz, blood pres, cardiac output, shock, female, t-2, swine, tox in vivo, cvp, iv

ABSTRACT

Overview:

EXPER-TOXICITY paper with stated purpose of CHARACTERIZE CARDIOVASULAR EFFECTS OF T-2 IN PIG reporting on 1 design(s).

Design Information:

Results: Design-Oriented

Design: 3 GRP, 3 EXP, Y CNTL

Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP

Exposure Regimen: T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE
VOMITING, PERSISTENT (3 —) in GASTROINTESTINAL TRACT, UPPER seen in 5/5 subjects with onset of ~1 HR hour(s) and duration of PERSISTANT hour(s).

SEVERE DIARRHEA, NOS in GASTROINTESTINAL TRACT, LOWER seen in 7/5 subjects with onset of ~1 HR hour(s) and duration of UNK hour(s).

UNK SEVERITY FLATULENCE in GASTROINTESTINAL TRACT, LOWER seen in 7/5 subjects with onset of ~1 HR hour(s) and duration of UNK hour(s).

CHEWING (— —) in MOUTH, NOS seen in 5/5 subjects with onset of < 0.5 HR hour(s) and duration of N/AV hour(s).

SALIVARY SECRETION, INCREASED (— —) in SALIVARY GLAND, NOS seen in 5/5 subjects with onset of < 0.5 HR hour(s) and duration of N/AV hour(s).

UNK SEVERITY RESTLESSNESS in BRAIN, NOS seen in 5/5 subjects with onset of UNK hour(s) and duration of UNK hour(s).

UNK SEVERITY STRAIN GAGE, BIOFEEDBACK in ABDOMEN, NOS seen in 37/5 subjects with onset of < 1 HR hour(s)

Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP

Exposure Regimen: ETHANOL 70%, N/AV, IA, given ONCE x ONE DOSE

No results reported for this Exposure Group.

Subjects: 5 PORCINE, Age: UNK , Wt: 50 KG, Sex: F, 1 EXP
Exposure Regimen: T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE
VOMITING, PERSISTENT (3 —) in GASTROINTESTINAL TRACT, UPPER seen in 5/5
subjects with onset of ~1 HR hour(s) and duration of PERSISTANT hour(s).

SEVERE DIARRHEA, NOS in GASTROINTESTINAL TRACT, LOWER seen in ?/5 sub-
jects with onset of ~1 HR hour(s) and duration of UNK hour(s).

UNK SEVERITY FLATULENCE in GASTROINTESTINAL TRACT, LOWER seen in ?/5
subjects with onset of ~1 HR hour(s) and duration of UNK hour(s).

CHEWING (— —) in MOUTH, NOS seen in 5/5 subjects with onset of < 0.5 HR hour(s)
and duration of N/AV hour(s).

SALIVARY SECRETION, INCREASED (— —) in SALIVARY GLAND, NOS seen in 5/5
subjects with onset of < 0.5 HR hour(s) and duration of N/AV hour(s).

UNK SEVERITY RESTLESSNESS in BRAIN, NOS seen in 5/5 subjects with onset of UNK
hour(s) and duration of UNK hour(s).

UNK SEVERITY DISORDER STRAIN GAGE, BIOFEEDBACK in ABDOMEN, NOS seen in
subjects

TKS Citation code: J00001-0009-00588-1987

File code: BEAS.9.588.87 in the following files: BP

(1422) Beasley VR, Lundeen GR, Poppenga RH, Buck WB: DISTRIBUTION OF BLOOD FLOW TO THE GASTROINTESTINAL TRACT OF SWINE DURING T-2 TOXIN-INDUCED SHOCK, FUNDAM APPL TOXICOL 9:588-594,1987

Keywords Assigned: radiolabel, blood flow, young, female, swine, tox in vivo, t-2

ABSTRACT

Overview:

EXPER-TOXICITY paper with stated purpose of STUDY GASTROINTESTINAL BLOOD FLOW IN T-2 TOXICOSIS reporting on 1 design(s).

Design Information:

Results: Design-Oriented

Design: 3 GRP, 3 EXP, Y CNTL

Subjects: 6 PORCINE, Age: N-AV , Wt: 55 KG, Sex: F, 1 EXP

Exposure Regimen: ETHANOL 70%, 7 ML, IA, given ONCE x ONE DOSE

No results reported for this Exposure Group.

Subjects: 6 PORCINE, Age: N-AV , Wt: 55 KG, Sex: F, 1 EXP

Exposure Regimen: T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE

No results reported for this Exposure Group.

Subjects: 6 PORCINE, Age: N-AV , Wt: 55 KG, Sex: F, 1 EXP

Exposure Regimen: T-2 TOXIN, 2.4 MCG/KG, IA, given ONCE x ONE DOSE

SEVERE VOMITING, NOS in GASTROINTESTINAL TRACT, UPPER seen in 3/3 subjects with onset of 1 HR hour(s) and duration of 4 HR hour(s).

TKS Citation code: J00217-0082-00532-1986

File code: COSG.82.532.86 in the following files: SLBP

(935) Cosgriff TM, Bunner DL, Wannemacher RW JR., Hodgson LA, Dinterman RE: THE HEMOSTATIC DERANGEMENT PRODUCED BY T-2 TOXIN IN CYNOMOLGUS MONKEYS, TOXICOL APPL PHARMACOL 82:532-539,1986

Keywords Assigned: other glycerol, water, car ethanol, plymph, gi, heart, gross, wbc, pcv-pvc, platelets, clot, clin ser enz, monkey, male, t-2, midage, hemmor, blood, rbc, lo

ABSTRACT

Overview:

EXPER-TOXICITY paper with stated purpose of DETERMINE EFFECTS OF T-2 ON BLOOD COAGULATION and implied purpose of PRIMATE MODEL FOR HUMAN EXPOSURE reporting on 1 design(s).

Design Information:

Results: Design-Oriented

Design: 1 GRP, 2 EXP, CNTL

Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP

Exposure Regimen: T-2 TOXIN, 0.65 MG/KG, IM, given x

UNK SEVERITY HEMORRHAGE, PETECHIAL in HEART, NOS seen in 3/5 subjects with onset of UNK hour(s)

UNK SEVERITY HEMORRHAGE, PETECHIAL in COLON, NOS seen in 3/5 subjects with onset of UNK hour(s)

UNK SEVERITY NECROSIS, NOS in LYMPH NODE, NOS seen in UNK subjects

UNK SEVERITY NEUTROPHILIC LEUKOCYTOSIS (T-0X160) in BLOOD NEUTROPHIL seen in UNK subjects with onset of 6 HR hour(s) and duration of 2 DAYS hour(s).

UNK SEVERITY LYMPHOCYTE PRODUCTION, DECREASED in BLOOD LYMPHOCYTE seen in UNK subjects with onset of 48 HRS hour(s) and duration of UNK hour(s).

LYMPHOCYTE PRODUCTION, INCREASED (20000 ML) in BLOOD LYMPHOCYTE seen in UNK subjects with onset of 6 HR hour(s) and duration of 18 HR hour(s).

UNK SEVERITY ACTIVATED PARTIAL THROMBOPLASTIN TIME in PLASMA seen in UNK subjects with onset of 12 HRS hour(s) and duration of ~3 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR II in PLASMA seen in UNK subjects with onset of 6-12 HR hour(s) and duration of 3 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR IX in PLASMA seen in UNK subjects with onset of 12 HRS hour(s) and duration of 2 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR V in PLASMA seen in UNK subjects with onset of 6-12 HRS hour(s) and duration of 1.5 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR VII in PLASMA seen in UNK subjects with onset of 12 HRS hour(s) and duration of >3DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR VIII in PLASMA seen in UNK subjects with onset of 12 HRS hour(s) and duration of 2-3 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR X in PLASMA seen in UNK subjects with onset of 12 HRS hour(s) and duration of 1.5 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR XI in PLASMA seen in UNK subjects with onset of 6 HRS hour(s) and duration of 3 DAYS hour(s).

UNK SEVERITY COAGULATION FACTOR XII in PLASMA seen in UNK subjects with onset of 6 HRS hour(s) and duration of 3 DAYS hour(s).

PROTHROMBIN TIME (MODERATE SECONDS) in PLASMA seen in UNK subjects with onset of 6 HRS hour(s) and duration of 2 DAYS hour(s).

No results reported for this Exposure Group.

System-Sign-Species-Sign-Dose-Study Design Monographs

Aflatoxin

LIPIDOSIS, NOS

(SEVERE) occurring in 5/5 subjects at with duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

ASPARTATE AMINO TRANSFERASE (SGOT) MEASUREMENT (F-23160)

(41IU/L) occurring in MEAN subjects at 14 DAYS with 14 DAYS duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

CREATINE KINASE (CK)

(109IU/L) occurring in MEAN subjects at 28 DAY with duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

GAMMA GLUTAMYL TRANSPEPTIDASE, SERUM, MEASUREMENT (GGT) (F-21340)

(29IU/L) occurring in MEAN subjects at 14 DAYS with 14 DAYS duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

LACTIC DEHYDROGENASE ISOENZYME, NOS

(277IU/L) occurring in MEAN subjects at 28 DAY with duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

PHOSPHORUS, DECREASED LEVEL

(SEVERE) occurring in MEAN subjects at 21 DAYS with 7 DAYS duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

DRY STRUCTURE

(MILD) occurring in 5/5 subjects at UNK with UNK duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures:AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design:5 GRP, 5 EXP, Y CNTL (2556)

ICTERUS, NOS

(SEVERE) occurring in 2/5 subjects at 25 DAYS with duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures: AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design: 5 GRP, 5 EXP, Y CNTL (2556)

CACHEXIA

(MILD) occurring in 5/5 subjects at UNK with UNK duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures: AFLATOXIN, 4 MG/KG, PO, given CHRON x 28 D Design: 5 GRP, 5 EXP, Y CNTL (2556)

NORMAL CONDITION

() occurring in 5/5 subjects at with duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures: AFLATOXIN, 2 MG/KG, PO, given CHRON x 28 D Design: 5 GRP, 5 EXP, Y CNTL (2556)

NORMAL CONDITION

() occurring in 5/5 subjects at with duration. Subjects: 5 PIG, Age: 6 W, Wt: 12 KG, Sex: C, 28 EXP Exposures: AFLATOXIN, 1 MG/KG, PO, given CHRON x 28 D Design: 5 GRP, 5 EXP, Y CNTL (2556)

REFERENCES

(2556) Harvey RB, Huff WE, Kubena LF, Corrier DE, Phillips TD: PROGRESSION OF AFLATOXICOSIS IN GROWING BARROWS, AM J VET RES 49:482-487, 1988

T-2 Toxin

HEMORRHAGE, PETECHIAL

(MILD) occurring in 3/5 subjects at UNK with duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

CHEWING

(—) occurring in 5/5 subjects at < 0.5 HR with N/AV duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

CHEWING

(—) occurring in 5/5 subjects at < 0.5 HR with N/AV duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

DIARRHEA, NOS

(3) occurring in ?/5 subjects at ~1 HR with UNK duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

DIARRHEA, NOS

(3) occurring in ?/5 subjects at ~1 HR with UNK duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

FLATULENCE

(UNK) occurring in ?/5 subjects at ~1 HR with UNK duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

FLATULENCE

(UNK) occurring in ?/5 subjects at ~1 HR with UNK duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

HEMORRHAGE, PETECHIAL

(MILD) occurring in 3/5 subjects at UNK with duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

SALIVARY SECRETION, INCREASED

(—) occurring in 5/5 subjects at < 0.5 HR with N/AV duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

SALIVARY SECRETION, INCREASED

(—) occurring in 5/5 subjects at < 0.5 HR with N/AV duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

VOMITING, NOS

(3) occurring in 3/3 subjects at 1 HR with 4 HR duration. Subjects: 6 PORCINE, Age: N- AV, Wt: 55 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 2.4 MCG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1422)

VOMITING, PERSISTENT

(3—) occurring in 5/5 subjects at ~1 HR with PERSISTANT duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

VOMITING, PERSISTENT

(3—) occurring in 5/5 subjects at ~1 HR with PERSISTANT duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

ACTIVATED PARTIAL THROMBOPLASTIN TIME

(MODERATE) occurring in UNK subjects at 12 HRS with ~3 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR II

(SIGNIF) occurring in UNK subjects at 6-12 HR with 3 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR IX

(MODERATE) occurring in UNK subjects at 12 HRS with 2 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR V

(MODERATE) occurring in UNK subjects at 6-12 HRS with 1.5 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR VII

(MODERATE) occurring in UNK subjects at 12 HRS with >3DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR VIII

(MODERATE) occurring in UNK subjects at 12 HRS with 2-3 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR X

(MODERATE) occurring in UNK subjects at 12 HRS with 1.5 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR XI

(MODERATE) occurring in UNK subjects at 6 HRS with 3 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

COAGULATION FACTOR XII

(MODERATE) occurring in UNK subjects at 6 HRS with 3 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

LYMPHOCYTE PRODUCTION, DECREASED

(MILD) occurring in UNK subjects at 48 HRS with UNK duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

LYMPHOCYTE PRODUCTION, INCREASED

(20000ML) occurring in UNK subjects at 6 HR with 18 HR duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

NECROSIS, NOS

(NOT STAT) occurring in UNK subjects at with duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

NEUTROPHILIC LEUKOCYTOSIS (T-0X160)

(MODERATE) occurring in UNK subjects at 6 HR with 2 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

PROTHROMBIN TIME

(MODERATESECONDS) occurring in UNK subjects at 6 HRS with 2 DAYS duration. Subjects: 12 MONKEY, Age: UNK ADUL, Wt: 4-6 KG, Sex: M, 1 EXP Exposures:T-2 TOXIN, 0.65 MG/KG, IM, given x Design:1 GRP, 2 EXP, CNTL (935)

RESTLESSNESS

(UNK) occurring in 5/5 subjects at UNK with UNK duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

RESTLESSNESS

(UNK) occurring in 5/5 subjects at UNK with UNK duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

S: RAIN GAGE, BIOFEEDBACK

() occurring in 32/5 subjects at < 1 HR with duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 0.6 MG/KG, IA, given ONCE x ONE DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

STRAIN GAGE, BIOFEEDBACK

DISORDER () occurring in subjects at with duration. Subjects: 5 PORCINE, Age: UNK, Wt: 50 KG, Sex: F, 1 EXP Exposures:T-2 TOXIN, 4.8 MG/KG, IA, given ONCE x ONE

DOSE Design:3 GRP, 3 EXP, Y CNTL (1410)

REFERENCES

(1422) Beasley VR, Lundeen GR, Poppenga RH, Buck WB: DISTRIBUTION OF BLOOD FLOW TO THE GASTROINTESTINAL TRACT OF SWINE DURING T-2 TOXIN-INDUCED SHOCK, FUNDAM APPL TOXICOL 9:588-594,1987

(1410) Beasley VR: EXPERIMENTAL T-2 TOXICOSIS IN SWINE I. CHANGES IN CARDIAC OUTPUT, AORTIC MEAN PRESSURE, CATECHOLAMINES, 6-KETO-PGF1ALPHA, THROMBANE B2, AND ACID-BASE PARAMETERS, FUNDAM APPL TOXICOL 5:879-892,1985

(935) Cosgriff TM, Bunner DL, Wannemacher RW JR., Hodgson LA, Dinterman RE: THE HEMOSTATIC DERANGEMENT PRODUCED BY T-2 TOXIN IN CYNOMOLGUS MONKEYS, TOXICOL APPL PHARMACOL 82:532-539,1986

Total Monograph

T-2 Toxin

T-2 TOXIN

CHEMICAL DATA: None available at this time.

UNK SEVERITY HEMORRHAGE. PETECHIAL seen in 3/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of UNK (935)

SEVERE VOMITING, NOS seen in 3/3 FEMALE, N-AV old N-AV PORCINE weighing 55 kilograms N-AV tallof GOOD; FEMORAL CATH health status (obtained from N-AV) which received a total of 1 exposure(s) to 2.4 MCG/KG T-2 TOXIN by PULMONARY ARTERY INF INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at EVERY 1.5 HR. Clinical effect had onset of 1 HR and duration of 4 HR. (1422)

VOMITING, PERSISTENT (3 —) seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of ~1 HR and duration of PERSISTANT. (1410)

VOMITING, PERSISTENT (3 —) seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of ~1 HR and duration of PERSISTANT. (1410)

SEVERE DIARRHEA, NOS seen in ?/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of ~1 HR and duration of UNK. (1410)

SEVERE DIARRHEA, NOS seen in ?/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of ~1 HR and duration of UNK. (1410)

UNK SEVERITY FLATULENCE seen in ?/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of ~1 HR and duration of UNK. (1410)

UNK SEVERITY FLATULENCE seen in ?/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of ~1 HR and duration of UNK. (1410)

CHEWING (— —) seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of < 0.5 HR and duration of N/AV. (1410)

CHEWING (— —) seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of < 0.5 HR and duration of N/AV. (1410)

SALIVARY SECRETION, INCREASED (— —) seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of < 0.5 HR and duration of N/AV. (1410)

SALIVARY SECRETION, INCREASED (— —) seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of < 0.5 HR and duration of N/AV. (1410)

UNK SEVERITY HEMORRHAGE, PETECHIAL seen in 3/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of UNK (935)

UNK SEVERITY NECROSIS, NOS seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. (935)

UNK SEVERITY NEUTROPHILIC LEUKOCYTOSIS (T-0X160) seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6

MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 6 HR and duration of 2 DAYS. (935)

UNK SEVERITY LYMPHOCYTE PRODUCTION, DECREASED seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 48 HRS and duration of UNK. (935)

LYMPHOCYTE PRODUCTION, INCREASED (20000 ML) seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of 6 HR and duration of 18 HR. (935)

UNK SEVERITY ACTIVATED PARTIAL THROMBOPLASTIN TIME seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 12 HRS and duration of ~3 DAYS. (935)

UNK SEVERITY COAGULATION FACTOR II seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 6-12 HR and duration of 3 DAYS. (935)

UNK SEVERITY COAGULATION FACTOR IX seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had

onset of 12 HRS and duration of 2 DAYS. (935)

UNK SEVERITY COAGULATION FACTOR V seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 6-12 HRS and duration of 1.5 DAYS (935)

UNK SEVERITY COAGULATION FACTOR VII seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 12 HRS and duration of >3DAYS. (935)

UNK SEVERITY COAGULATION FACTOR VIII seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 12 HRS and duration of 2-3 DAYS. (935)

UNK SEVERITY COAGULATION FACTOR X seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 12 HRS and duration of 1.5 DAYS. (935)

UNK SEVERITY COAGULATION FACTOR XI seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 6 HRS and duration of 3 DAYS. (935)

UNK SEVERITY COAGULATION FACTOR XII seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of 6 HRS and duration of 3 DAYS.(935)

PROTHROMBIN TIME (MODERATE SECONDS) seen in UNK FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effects had onset of 6 HRS and duration of 2 DAYS.(935)

UNK SEVERITY RESTLESSNESS seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of UNK and duration of UNK. (1410)

UNK SEVERITY RESTLESSNESS seen in 5/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of UNK and duration of UNK. (1410)

UNK SEVERITY STRAIN GAGE, BIOFEEDBACK seen in 37/5 FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 0.6 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. Clinical effect had onset of < 1 HR (1410)

UNK SEVERITY DISORDER STRAIN GAGE, BIOFEEDBACK seen in FEMALE, UNK old CROSSBRED PORCINE weighing 50 kilograms of GOOD; FEMORAL CATH health status (obtained from UNK) which received a total of 1 exposure(s) to 4.8 MG/KG T-2 TOXIN by PUMPED IN OVER 5 MIN INTRA-ARTERIAL INJ route every ONCE for a duration of ONE DOSE. The subjects were evaluated at CONTINUOUSLY. (1410)

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Appendix G. Toxin Knowledge System Documentation

Note that the Documentation has its own page number sequencing and table of contents.

Toxin Knowledge System Program Documentation

Version 7.11g5b1a

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Note to Users!

Please assist us by communicating anytime something doesn't work as described, or is not clear in this manual. Please feel free to make suggestions! You can contribute to the development and improvement of the program and its documentation. If you are located at the College of Veterinary Medicine, University of Illinois at Urbana-Champaign, messages can be left in our mailbox in room 1220, Veterinary Medicine Basic Sciences Building. We can be called at (217) 333-2053, or be sent electronic mail at htrammel@iapic.cvm.uiuc.edu.

Thank you,
Harold L. Trammel, Pharm. D., Richard J. Lambert, Ph.D., D.V.M.
TKS Development Team
December, 1989

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1

Program Overview

What is commonly called the "information explosion" has made it increasingly difficult to keep up with what is being published internationally, and to integrate and synthesize what is being done by numerous individual researchers. Even if the focus of interest is very narrow, it is often difficult to understand the meaning of experimental findings and how they relate to one another because there are so many different experimental variables. Each research group has a particular question they are trying to address. Even if one or more groups have the same question, they will go about answering it in very different ways. The following list includes some of the parameters that may differ: animal model, agent preparation methods and dosing formulations, duration of exposure, evaluation parameters and interpretation of results.

The concept of this program is to take the detailed information that is commonly given in written reports, break it down into component parts and place it within a consistent framework in a relational database. One can then ask general or specific questions of the database instead of studying each paper, making comparisons. Since the TKS system was initially developed using mycotoxin literature, we will use them as an example.

Suppose you wanted to identify the mycotoxins which were associated with kidney lesions in swine. The database could be asked for a list of citations in which swine were the subjects and where kidney lesions were found. It should also be possible to identify reports where a specific type of kidney lesion was reported, such as proximal tubular degeneration. As you can see, it is also possible to use the database as a diagnostic tool. What toxin is associated with causing cardiac lesions, elevated body temperature and decreased circulating neutrophils?

What does this give you that cannot be obtained from other citation databases? Well, you can also ask the TKS database to give you information about the material and methods sections of the citation matches so that you can compare the agent formulations, doses administered, route of administration and duration of exposure, as well as other parameters which may have influenced the results or their frequency of occurrence. The differences in experimental protocols could be used to explain variability in results and suggest unifying experiments.

The TKS system provides another tool for information management. Scientists will typically base their reprint files on particular subject groupings or alphabetize them based on the authors names. The TKS system provides a classification scheme and a way to locate information which utilizes both approaches. You can locate work done by certain people, yet perform searches looking for specific topical information.

Having the information available on a magnetic medium means that others with a terminal and connect permission may also have access to the information. The data is available in an abbreviated but detailed form to many. One can maintain a main repository or several component repositories for hard copies of the original manuscripts for reference purposes.

Although it was originally conceived as a mini or mainframe product to handle large amounts of data. The program is being ported to MS-DOS compatible microcomputers and perhaps to the Macintosh platform. This means that potential users could establish their own databases centered around the topics important to them on their own machines.

Documentation Overview

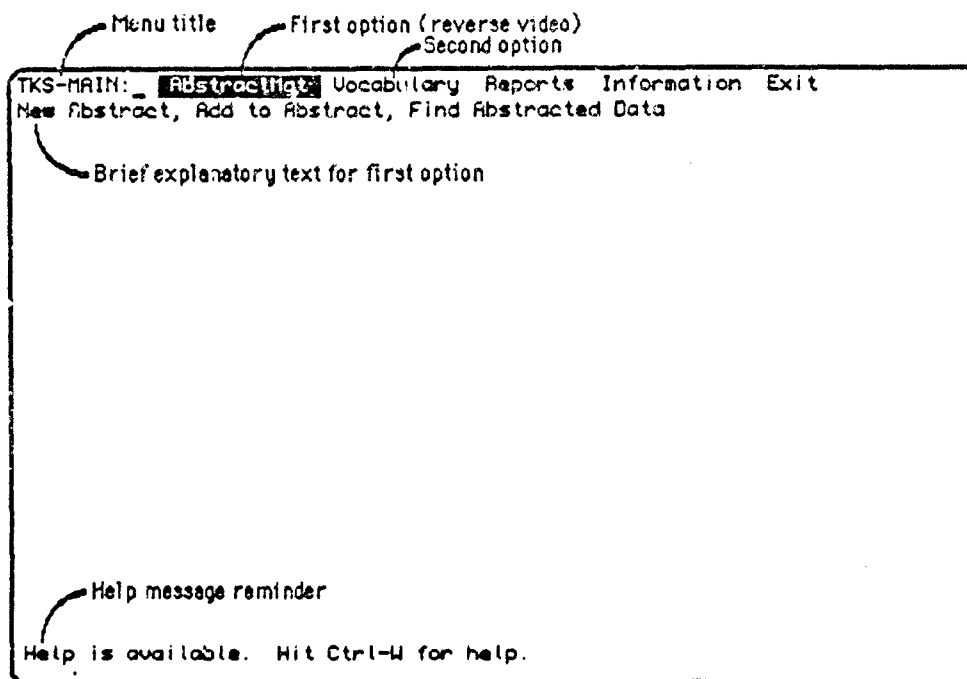
You can learn to use the Toxin Knowledge System by following the program documentation sequentially, starting at TKS-MAIN: Menu Options. You will be taken through the process of entering data from an article by first defining the citation data and paper overview, and later the other component parts such as the materials and methods (study design, subject groups, treatment regimens), results and discussion.

TKS-MAIN Menu

TKS-MAIN Menu Options

When the TKS-Program is started, the "TKS-MAIN" menu options are available (Figure 1.1). The first option in the list is selected as indicated by the reverse video (highlight or funnel enclosure on some screens) of "AbstractMgt." You can move through the menu by using the right and left arrow or cursor keys. Messages which briefly explain each option appear below the menu.

Figure 1.1
TKS-MAIN
Menu and
Screen bar.



In addition, on-screen help messages are available for most menu items and can be accessed by hitting the "control" and "w" keys simultaneously (Ctrl-w).

Study Figure 1.1 and read the next few paragraphs before trying anything.

You may invoke the desired menu option by typing in lower case the first letter of the option you wish to select or by hitting "return" when an option is highlighted. For example, typing "e" will select the "Exit" option. However, this method may not allow you to see the brief explanatory text associated with each option.

AbstractMgt

Selecting the first option in the TKS-MAIN menu brings you to the "ABSTRACT" menu where abstracts can be entered, abstracts already entered can be added to (completed), or modified in some other way, or where searches for abstracted information can be performed. Documentation for this path begins below.

Vocabulary

This option allows access to the lists and codes for journals, books, keywords, clinical findings and chemical vocabulary. These areas can be browsed, modified, added to or searched.

Reports

This option displays the "Report" menu with two choices available at this time. This menu has just begun to be utilized but is not yet "on-line." Eventually this is where a user can view the most current monographs, generate new monographs (report summaries), generate structured abstracts for a specific paper, and use other features yet to be developed.

Information

Choosing this option brings the user to the "INFORMATION" menu which currently has two menu choices. They are "Copyright" and "Development." Copyright brings up the copyright notes and the program version number as well as a summary of the stages of development of the individual programs which form the *Toxin Knowledge System*.

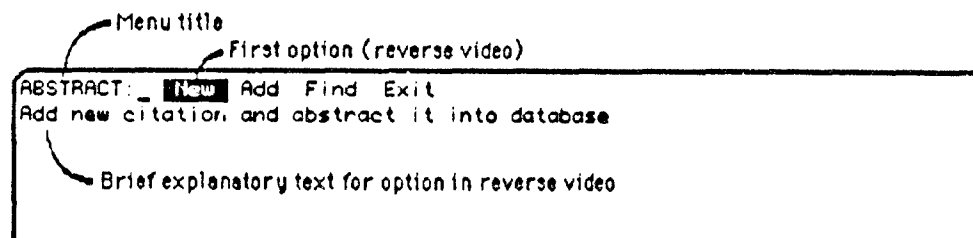
Exit

Selecting "Exit" removes you from the TKS program if you are in the first menu (TKS-MAIN), and moves you to the previous menu if you are at any other point in the program.

ABSTRACT Menu Options

Select "AbstractMgt" and a new menu appears, entitled "ABSTRACT." The options presented (Figure 1.2) are "New," "Add," and "Find." Selecting "New" from this menu begins the process of entering a new citation. The "Add" option (see Chapter 7) allows you to add components to an already entered abstract. This frequently occurs when citation information has been entered but the content of the paper (materials and methods, subject group descriptions, etc.) has not been abstracted. Choosing the "Find" option allows you to search for various aspects of entered papers.

Figure 1.2
ABSTRACT
Menu and
Screen



New

The selection of the "ABSTRACT" menu choice "New" begins a series of screens which take the user through the entry process for a new document (journal article or book chapter) into the system. First, the user will enter citation data (Figure 1.3), followed by the author and keyword information, paper content, comments, etc.

Citation Data Information

Figure 1.3
CITATION
DATA SCREEN

Selecting this option brings up the screen below

```

ABSTRACT:  New Add Find Exit
-----
CITATION DATA SCREEN
|Citation No:[          ] File No:[          ]|
|Source:[          ] File Loc.:[          ] Entry Date:[          ]|
|Volume/Chap:[          ] Pages:[          ]-[-] Year:[          ]|
|Title:|
| |
| | Please enter last name of first author |
| |
| |
|Journal/Book Title:|
| |
|Authors [0] Keywords [0]|
|PaperOver [0] Design [0] Subjects [0] ExpoReqs [0] Signs[0]|
|
|
-----
Help is available. Hit Ctrl-W for help.
    
```

Author

After the CITATION DATA SCREEN is displayed, a dialog window appears and prompts you for the last name of the first author (you do not need to type upper case letters). Enter the author information, then hit the "return" key.

Source

You are then asked for the journal (or book) "source code" which is a 5 digit number with a "J" (or "B") prefix, for example, "J00217."

NOTE! If you make a mistake and wish to abort an entry, use the "Del" (delete) key. A misspelling can be corrected using the "Backspace" key.

TKS JOURNAL-LIST (J-LIST) Menu

Find

Select "Find" and type what you believe the correct abbreviation would be for that journal. As an example, type "TOX APPL PHARM" and hit the "escape" key (Esc). The program searches for a match. As you can see, sometimes one is not found. When this occurs you can try another option, or use an aid such as a "wild card" (*).

```

ABSTRACT:  New Add Find Exit
+-----+
| Enter source code | J-LIST:  Find Add Select Exit | | | |
|                   | JOURNAL SOURCE LIST |
| Citation No.: [ ] | | | | |
| Source: [ ] | | | | |
| Volume/Chap: [ ] | | | | |
| Title: | | | | |
| [ ] | | | | |
| [ ] | | | | |
| [ ] | | | | |
| [ ] | | | | |
| [ ] | | | | |
| Journal/Book Title | | | | |
| [ ] | | | | |
| [ ] | | | | |
| Authors (0 ) | | | | |
| Paper Over (0 ) | | | | |
| [ ] | | | | |
+-----+
Help is available. Hit Ctrl-W for help.

```

5

Figure 1.5
JOURNAL
SOURCE LIST
Screen after
search using
"TOX"

ABSTRACT: **Del** Add Find Exit — List identified after search using "TOX"

J-LIST: **Find** Add Select Exit

Enter source code: Highlight a journal abbreviation and press ESC

JOURNAL SOURCE LIST

Citation No: []	[] TOXICOL APPL PHARMACOL	[] J002171
Source: []	[] TOXICOL EUR RES	[] J002211
Volume/Chap: []	[] TOXICOL LETT	[] J002181
Title: []	[] TOXICOL PATHOL	[] J002221
[]	[] TOXICOL VITRO	[] J005951
[]	[] TOXICOLOGIST	[] J003811
[]	[] TOXICOLOGIST-ABSTR 1985 MEET	[] J005427
[]	[] TOXICOLOGY	[] J002231
[]	[] TOXICON	[] J000002
Journal/Book Title	[] TOXICON (SUPPL)	[] J005101
[]	[]	[]
[]	[]	[]
Authors (0)	[]	[]
PaperOver (0)	[]	[]
[]	[]	[]

Help is available. Hit Ctrl-W for help.

Since there is a good chance that the article you are trying to abstract is not in the above list, you can abort the process by hitting the delete (Del) key. The cursor returns to the J-LIST menu, where you can repeat the procedure to find the source code for the journal of interest.

When you have completed the "Source Code" field, hitting the "return" key will move the cursor to the next field.

If the journal you are abstracting already has a source code, you may skip the section below and go directly to "File Loc." several paragraphs further down.

Add

This option is used to add new journals or books to the source code list. Type "a" and the TKS JOURNAL SOURCE DATA SCREEN pops up with the cursor on the "Journal Name" field.

Figure 1.6
JOURNAL
SOURCE
DATA SCREEN

ABSTRACT: New Add Find Exit		CE LIST
JOURNAL SOURCE DATA SCREEN		
Acquisition Number: []	
Journal Code: []	
Journal Name:		
[]	
[]	
Journal Abbreviation:		
[]	
[]	
[]	
[]	

Help is available. Hit Ctrl-H for help

It is the same screen as the one that can be accessed by selecting the "Vocabulary" option from the "TKS-MAIN" menu and "Journals" from the subsequent "VOCABULARY" menu. See the "Vocabulary" section for an explanation of the options.

Type in the journal name followed by "return," until the next field is reached. Type in the journal abbreviation (obtained from the *National Library of Medicine List of Journals Index*) and then "Esc," which causes the entry to be assigned an "Acquisition Number" which is given out sequentially, and a Journal Source Code, which is based on the Acquisition Number. The program automatically enters the new source code for the journal in the appropriate field in the CITATION DATA SCREEN.

Select

Choosing "Select" will serve no purpose unless you have a list of journals from which one needs to be selected. When a list is available, one can invoke this option by choosing it and then hitting "Esc" as requested on-screen.

Figure 1.7
CITATION
DATA SCREEN
Completed via
the "New" path
from the
"ABSTRACT"
menu.

```

ABSTRACT:  New Add Find Exit
-----
CITATION DATA SCREEN
Citation No: [000217-0100-00100-1989] File No: [101 100 00 89]
Source: [000217] File Loc: [ ] Entry Date: [12/05/1989]
Volume/Chap: [100] Pages: [100 1-150] Year: [1989]
Title:
[THIS IS AN EXAMPLE FOR DOCUMENTATION PURPOSES]
Journal/Book Title:
[TOXICOL APPL PHARMACOL]
Authors [0] Keywords [0]
PaperOver [0] Designs [0] Subjects [0] ExpoRegn [0] Signst [0]
-----
Help is available. Hit Ctrl-H for help.
    
```

File Loc.

"File Loc." (Figure 1.3) is short for file location. This provides a way to indicate where a specific file may be located, and is particularly useful when files may be stored in several different locations. If one wants to locate a particular file, this field in TKS citation can be used to identify where to look (hopefully, it will be there).

Since there is space for only 6 characters, abbreviations can be set-up for particular places or names of individuals. Type in the location of the citation or book and hit "return."

If you do not wish to use this option hit "return" to move to the next entry point.

Volume/Chap

Enter the of the journal or the number of the book chapter from which the article was taken. Hit "return" to move to the next field.

Pages

Enter the beginning page number followed by a "return," and the ending page number and "return."

Year

Enter the year in which the citation was published, *using all four digits*, then "return." If you are not in a hurry, try entering just the last two digits of the year and "return." See what happens? Completing this field correctly provides the program with the final bit of information necessary to construct the citation number ("Citation No."), which now appears.

Citation No. and File No.;

The citation number consists of the journal source code (6 spaces), the volume or chapter number (4 spaces), the beginning page number (5 spaces) and the year (four digits). All items must be separated by hyphens. The number must include characters in all of the spaces allotted, meaning that zero's (0, not the letter O) should be used to fill in blank characters at the beginning of a number. Each field is separated by a hyphen. The following is an example, showing the blank characters underlined: J00033-0052-00167-1988.

Typing "return" again, fills in the "File No." field automatically. It consists of the first four letters of the first author's last name, the journal or chapter number, the beginning page number and last two digits of the year. This number may also be used to find the file after it is in the system. It does not consist of extra characters or spaces. There are periods separating portions of the entry. The following is an example, SMIT.33.52.167.88.

Hit "return" again.

If the citation you are attempting to enter is already in the system, you will receive notification of that fact. You may make changes in a file that is already in the system, but not from the "New" citation pathway. This will be explained in a later section. If the citation data has already been entered, you can check to see if other components have been entered and either add them or "Exit" back to the "ABSTRACT" menu and begin the entry process again for another article.

If the citation you entered is new, the "return" following the "File No." will bring the cursor to the title entry.

Title

Enter the title of the article (type in small case) with no period. There is room for even lengthy titles. They will not automatically wrap around the allotted space. As a result, words may be split at the end of lines. Do not attempt to prevent this. The program does not correct spelling, so check your entry. Once the title is complete so is this screen, so hit "Esc," which causes what you typed to be written to memory.

Note! Useful keys for correcting misspellings are the "Control-x" sequence to erase a letter and "Control-a" to insert characters

AUTHOR DATA SCREEN

During the initial entry process for a new citation, the Author screen comes up after the title entry (see Figure 1.8). Enter the last name, a space and initials (no space between initials) of the first author as requested in the note on the bottom of the screen. Hit "return" and the cursor moves to the "AuthSig" area where you can enter the position of the author in the sequence of names on the publication. The program will enter the numbers if you enter the names in the proper order. Just hit "return" when the cursor is in the "AuthSig" field. You can add up to six names to the author list.

Figure 1.8
AUTHOR
DATA SCREEN
(Overlay)

```

ABSTRACT:  New Add Find Exit

CITATION DATA SCREEN
Citation No: 100217-0100-00100-1989  File No: 101 100 100 60
Source: 100217  File Loc: 1  Entry Date: 12/05/1989
Volume/Chap: 100  Pages: 100 1-150  Year: 1989
Title:
(THIS IS AN EXAMPLE FOR DOCUMENTATION PURPOSES)

AUTHOR DATA SCREEN
Citation: 100217-0100-00100-1000  Citfile: 101 100 100 60
Author:  AuthSid:
Last Name, space, Initials; no punctuation

```

When you are finished, hit "Esc" once again. This writes to memory the author list and the keyword screen pops up.

KEYWORD DATA SCREEN

KeyCodes and Keywords can be used to enter specific information on any aspect of a paper. Clinical signs, physical signs, gross pathology, clinical pathology and histopathology findings, toxin preparation methods, animal treatment information, statistical analysis or any other component of a report.

Figure 1.9
KEYWORD
DATA SCREEN
(Overlay)

The screenshot displays a terminal window titled "ABSTRACT:". At the top, there are menu options: "New Add Find Exit". The main area is divided into two sections by dashed lines.

Left Section:

- Citation No.: [000217-0100-0v]
- Source: [000217] File
- Volume/Chap: [100] Page
- Title: [WAS IS AN EXAMPLE FOR ...]
- Citation: [000217-0100-0v]
- Author: [RAMMSI H]

Right Section:

- KEYWORD DATA SCREEN
- Citation: [000217-0100-0100-1989]
- Citfile: [RAM: 100: 100: 39]
- KeyCode: []
- Keyword: []

A large rectangular box on the right side contains instructions:

```
Enter keywords here
If you do not know
the correct code,
type "X" in the
"KeyCode" field,
followed by "return."
```

At the bottom of this box, it says: "When finished, hit 'Esc' to write this information to memory."

Keywords provide more than ancillary information. They can be used to search for certain papers that meet particular criteria. Which papers report effects of toxin "X" in monkeys? Who gave feed contaminated with purified toxin? cultured extracts? Which papers reported the use of fasted mice and which allowed access to food up until the time of dosing? Do young animals react differently than older ones?

KeyCodes are used to simplify the entry process by decreasing the number of key strokes needed to enter a description.

The current keywords were designed primarily for use with journal or book articles describing toxicologic studies with mycotoxins, though they should also be suitable for describing work with other toxins. They are arranged by major headings (toxin type, species, exposure route, etc.).

NOTE: The KeyCode/Keyword portion of the TKS system is in an early stage of development.

KeyCodes and Keywords

Enter the appropriate keycode(s) and hit "return." The keywords now appear to the right. Hit "Esc" to write them to memory.

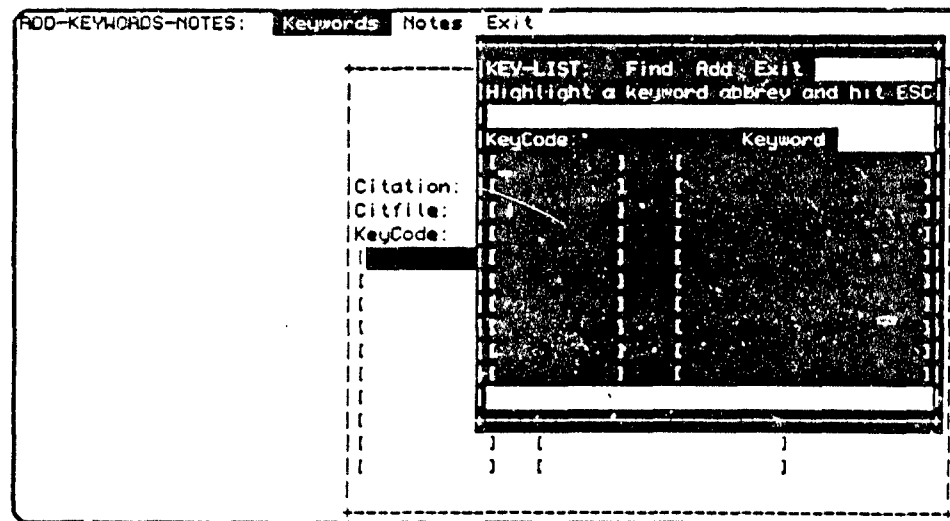
If you do not wish to enter keywords at this time, hit the "delete" key.

Since you do not know any of the keycodes, enter a code of "C02" and press "return." The keyword matching that code is placed in the next field. If one knows the keycodes, this is the quickest way to enter them. Currently, it may be useful to have a hard copy of the Keycodes and Keywords in order to look the Keywords up "manually" by major heading and group.

If an incorrect entry is placed in the "Keycode" field followed by a "return," or you hit the "delete" key, the program *assumes* you need help, and brings up the *KEY-LIST SCREEN*.

KEY-LIST SCREEN

Figure 1.10
KEY-LIST
SCREEN



KEY-LIST Menu

Find

The "Find" option helps you search for particular keywords that are in the list, and identifies their associated keycode.

Type "f" and the cursor is placed on the first field (KeyCode). Hit "return" and the cursor goes to the "Keyword" field. Type in the word "mouse" and hit "Esc." The program searches for that keyword and, if it is found, fills in the keycode number. One can enter that KeyCode and Keyword combination in the *KEYWORD DATA SCREEN* by hitting "Esc" once again when the desired pair is highlighted. From there, the process starts over for the next keyword.

If a keyword is searched for but not found, the program responds with a message that "There is no keyword matching the first three letters" and returns you to the *KEYWORD DATA SCREEN*.

Add

The "Add" option allows the freedom to place new keywords and their accompanying codes into the KEY-LIST. Selecting it brings up the *KEYWORD VOCABULARY SCREEN* with the cursor in the "KeyCode" field. In order to complete the process for a new Keyword, you need to know the KeyCodes for the other Keywords in order not to alter already established associations. Enter the appropriate KeyCode, and associated Keyword, followed by "Esc."

Figure 1.11 *KEYWORD VOCABULARY SCREEN*

```
KEYWORD LISTING:  Add Find Exit
Add Keyword to Keyword Vocabulary

                                KEYWORD VOCABULARY SCREEN

      KeyCode:                Keyword:
      [                    ] [                    ]
```

(If you do not wish to enter new keywords at this time, hit the "delete" key. If you follow this later path, the screen indicates that it is preparing citation "information.")

CURRENT PAPER Menu

The next menu is titled "CURRENT PAPER" and has only one option, "Exit." That is because you are finished with the first part of the system and must begin a new phase of data entry for the citation. Note that the screen provides a summary of what citation information has been entered so far, including keywords. Hit "e" or "return" to go on.

Figure 1.12
CURRENT
PAPER Menu

```

CURRENT PAPER:  Exit
J00217-0100-00100-1989      TRAM.100.100.89
TRAMMEL HL,: THIS IS AN EXAMPLE FOR DOCUMENTATION PURPOSES, TOXICOL APPL PH
ARMACOL 100:100-150,1989 , rat, path clin, tox in vivo

```

You are then asked if you would like to "add content data ... for this paper?" Content refers to data components such as Paper Overview, Designs, Subjects, Regimens, etc.

Figure 1.13
Query prior to
entering
additional
citation data

```

Do you want to add content data to system for this paper? (Y/n)

```

If you type "n" then "return," you have completed the citation data portion of the entry process and will be returned to the "ABSTRACT" screen. Typing "y" followed by "return" results in a new screen which begins the paper overview process.

Return to TKS-MAIN Menu

TKS-MAIN Menu: Vocabulary

Following this path brings up the "VOCABULARY" menu which allows one to work with the Journal, Book, Keyword, Sign, and Chemical lists.

VOCABULARY Menu

Journals

Selecting "Journals" brings up the JOURNAL-VOCABULARY menu, with options to "Add" journals to the list, "Find" a particular journal, or "Exit" from the program.

JOURNAL-VOCABULARY Menu

Add

Selecting "Add," puts the cursor on the "Journal Name" field. Type in the journal name as given in the *National Library of Medicine List of Journals Index*, and hit "return" until the "Journal Abbreviation" field is reached and enter the appropriate abbreviation as given by that Index. Hit "Esc" and the journal is assigned a Journal Code Number. The numbers are unique to each journal, and assigned sequentially.

Find

Selecting "Find," puts the cursor in the "Journal Code" field. More commonly you will need to use the "Journal Name" field, so hit "return" to place the cursor there and type in the EXACT name of the journal in order to find its journal code. If you typed the name correctly and it is already in the system, the remaining information for that entry is now provided on-screen. If there is no match, check your spelling and title. If they are correct, and there is no match, you will have to enter it as a new journal via the "Add" feature. Go back to the JOURNAL-VOCABULARY screen and follow the "Add" path (see above).

You do not have to type in the whole name of the journal, you can use the first few letters of the first word, or the first word or two and a "wild card" symbol (*). For example, type in "American*" and hit "Esc." The message at the bottom left corner of the screen tells you that more than one match was found. Increasing the length of the search pattern will decrease the number of matches you obtain.

You can now "cycle" through the matches by using the first four options indicated in the "BROWSE" menu near the top of the screen. Hitting "n" for next, or "return" when next is highlighted or surrounded by quotes brings up the next entry in the list. An "l" will bring you to the last match found. By using the right and left arrow keys you can cycle through the "BROWSE" menu and obtain a brief description of each option.

Books

The "Book" list portion of the TKS system is not yet fully operational.

Keywords

Use of this option is described under Keywords for a "New" citation.

Signs

This portion of the program is not yet operational.

Chemicals

This portion of the program has not yet been implemented.

2

Paper Overview Entry

PAPER OVERVIEW SCREEN

The PAPER OVERVIEW SCREEN begins the paper content entry process. Following this screen, the user will be taken through sequential screens in order to enter data about different components of the paper's content. Currently the user will see this screen, the STUDY DESIGN DATA SCREEN, SUBJECT GROUP DATA SCREEN, EXPOSURE REGIMEN DATA SCREEN, and the EXPOSURE GROUP LINK ENTRY SCREEN.

Hit "return" until the cursor is in the "Stated Purpose" field.

Figure 2.1
PAPER
OVERVIEW
SCREEN

Hit RETURN to add data.

PAPER OVERVIEW SCREEN

Citation Num: [000217-0100-00100-1989] File No: [EXAM:100:100:89]

Stated Purpose: [USE AS AN EXAMPLE FOR DOCUMENTATION PURPOSES]

Implied Purpose: [SAME]

Paper class: []

Number of Study Designs in Paper: []

E = Experimental
N = Non-Experiment
I = Info Only
C = Combination

Menu option choices for the first field of "Paper class." You must select one of the four letters.

Stated Purpose

There is room here to succinctly identify the stated purpose of the paper or book. That is, the purpose *as stated by the authors*. There are 50 spaces. Type in the stated purpose followed by "return."

Implied Purpose

One can often identify information which hints at a purpose not specifically stated. For example, researchers may study the effects of an expensive toxin on mice because they do not have enough material to use on a larger animal that may be more closely related to the target population, people. Perhaps, the long term effects of a toxin such as cadmium was the primary interest, but animals were only fed contaminated diets for 2 weeks because they developed a viral infection and began to die.

Toxin Knowledge System Documentation

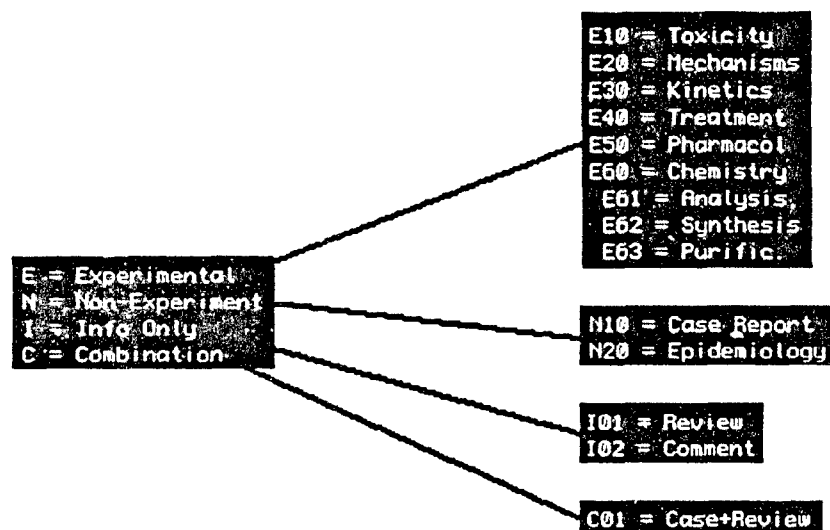
Type in the implied purpose followed by "return." If there is none, leave it blank (hit "return").

Paper Class

Select one of the descriptors from the pop-up menu on the right side of the screen (see Figure 2.1) by typing the indicated letter in the space provided.

The cursor moves to the second field for "Paper Class" and the descriptors change. Enter the appropriate classification (see Figure 2.2) and wait for the cursor to move to the next field.

Figure 2.2
Options
available for
the "Paper
class" fields



Number of Study Designs in Paper

This may be simply stated in the manuscript, but more often you will have to carefully check the material and methods section (and sometimes the Results and Discussion) to determine the number of designs used in the experiments described. Usually there will be a single study design for each particular question or hypothesis. Defining the study design goes hand in hand with determining the questions being asked. Good researchers will specifically state their hypotheses and this, in turn, will help you in entering their paper into the database.

You may use the arrow keys or the "return" key to cycle through portions of this screen if the need arises. You might think of a better way to express the implied purpose, or you may have made an error that needs to be corrected.

Remember, useful keys for correcting misspellings are the "Control-x" sequence to erase a letter in an entry, and "Control-a" to insert characters.

Enter the number of designs and hit "Esc," since you are done with this screen. The STUDY DESIGN DATA SCREEN comes up next.

3

Study Design Data Entry

STUDY DESIGN DATA SCREEN

Below the title of the *STUDY DESIGN DATA SCREEN* you can see the number of the study design you will be entering and the total number of designs as indicated from the *PAPER OVERVIEW DATA SCREEN*. The number of designs will increment as additional screens are entered up to the maximum number of designs indicated in the paper overview screen. When the maximum number is reached, the design screen will disappear and the next part of the process begins.

The screen comes up with the cursor on the "Type of Study" entry field.

Type of Study

Enter a selection from the menu to the right by typing the corresponding abbreviation, followed by "return."

Figure 3.1
STUDY
DESIGN DATA
SCREEN

Hit RETURN to begin to add data.

STUDY DESIGN DATA SCREEN

Citation No: [000217-0100-00100-1989] File No: [EXAM:100:100:89] Design No. [1] of [1]

Type of Study: [] []

In Vivo or In Vitro: [] []

Controls (y/n): []

Comparison Info: [] []

Comparison Methods: [] []

Control Methods: [] []

Control Types: [] []

How were subjects assigned to their groups? [] []

Numb. of Subject Groups: []

Numb. of Exposure Regimens: []

Screen menu options for the "Type of Study" field. You must enter one of the letters matching an option.

A = Survey
A1 = Prospective
A2 = Retrospective
B = Experiment
C = Therapeutic
D = Prophylactic
E = Symptomatic
F = Case Report

Note! You can move through the different fields in this screen by using the arrow and/or return keys. This is particularly useful if you find that an error has been made and you need to edit a previous field.

The type of small menu selection screen which comes up after an entry depends on the response in a previous field. For example, if you indicated earlier in the *PAPER OVERVIEW SCREEN* that the paper being entered was an "Info only" paper, then you would not have been able to indicate there were study designs, since those sorts of papers do not generally include experiments (experiments have, or at least should have, designs).

With the current screen, if you indicate that there are no controls, then you will not be able to enter the fields from "Comparison Info" on down.

In Vivo or In Vitro

Again, select from the menu to the right side of the screen and type in the designation for the appropriate classification, and the cursor will move to the next field. The choices for this field are illustrated below.

Figure 3.2
Choices for In
Vivo or In Vitro
field



Controls (y/n)

Enter "y" if negative or positive controls were used in the experimental design and "n" if they were not .

Comparison Info

If the answer to the above is "y," then you will be able to enter information in this and the following fields. Type the correct letter from the pop-up menu and hit "return" (see the following page for a representation of the options available)."

Comparison Methods

Type the appropriate letter and number (see the following page for a representation of the options available).

Control Methods

Type the proper letter and hit "return" (see the following page for a representation of the options available). No "return" is necessary

Control Types

Type the correct letter and number (see the following page for a representation of the options available).

How were subjects assigned to their groups?

Type the appropriate letter followed by a "return" (see the following page for a representation of the options available).

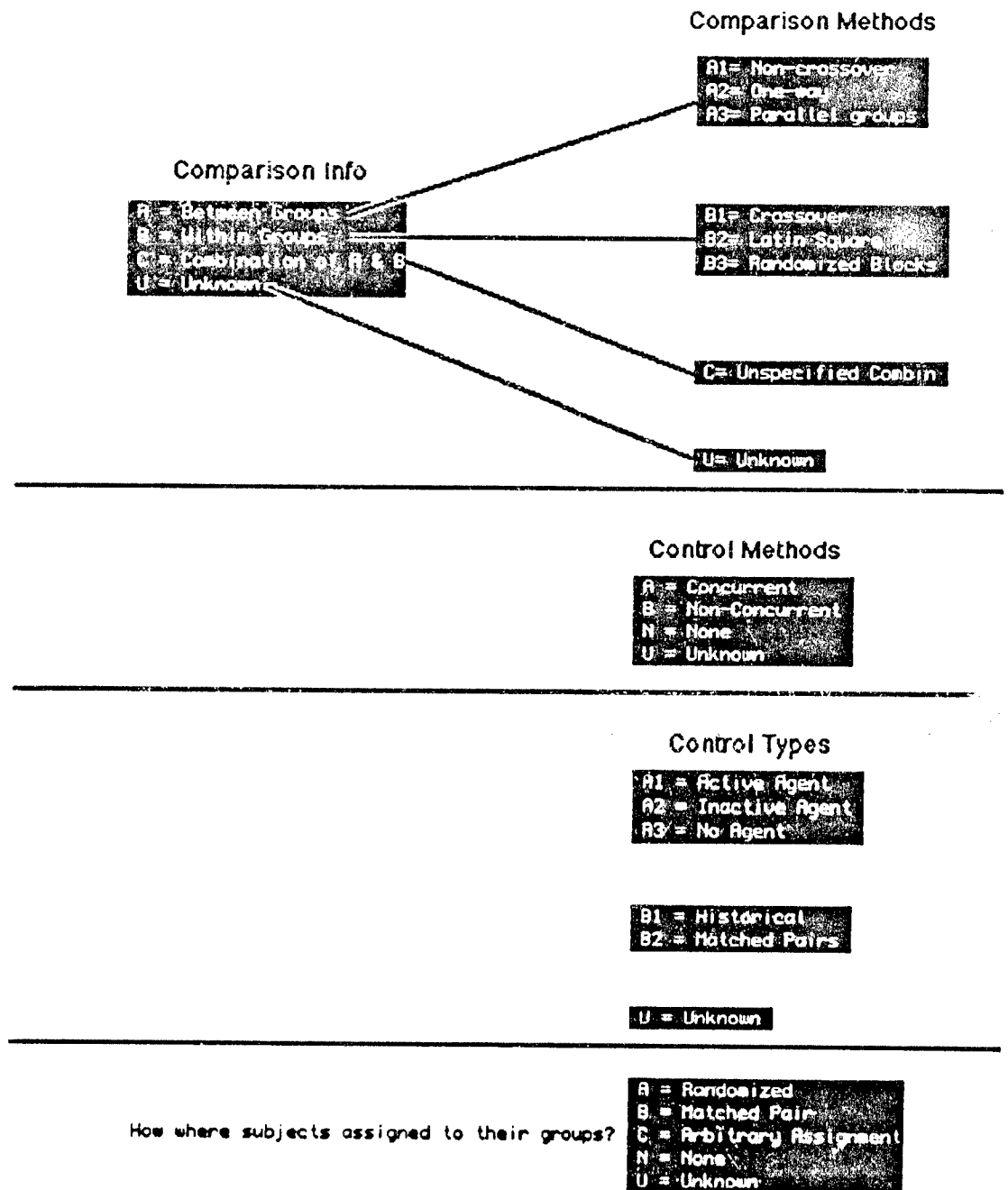


Figure 3.3 Summary of Options Available for the fields of the STUDY DESIGN DATA SCREEN

Number of Subject Groups

Examination of the report is necessary to determine the appropriate response here. Please note that the number of subject groups encompassing the current design should be entered! Other designs will have their own subject groups. Enter the number and then "return." This brings up the first *SUBJECT GROUP DATA SCREEN*. It will be followed by additional *SUBJECT GROUP DATA SCREEN(s)* if you indicated that there were multiple subject groups for a particular design. Hit "return" to automatically enter the "Citation No." and move the cursor to the first data field.

Number of Exposure Groups

As each *SUBJECT GROUP SCREEN* is completed one is given the opportunity to indicate how many *exposure* groups are associated with each *subject* group. For example, one subject group may consist of 60, 30-day old male Sprague Dawley rats exposed to a diet containing lead at a concentration of 10 ppm (30 animals) or a control diet with 0.05 ppm (background concentration) of lead. The two treatments, 10 or 0.05 ppm lead, constitute two exposure groups.

4

Subject Group Data Entry

SUBJECT GROUP DATA SCREEN

When this screen appears the number designation of the subject group you will be entering and the total in that particular design are indicated below the SUBJECT GROUP DATA SCREEN.

Figure 4.1
SUBJECT
GROUP DATA
SCREEN

```

Enter search criteria and hit ESC to search
SUBJECT GROUP DATA SCREEN
Citation No. [ ] of [ ] of Design [ ] [ ]
Group [ ] of [ ] of Design [ ] [ ]
Species [ ] Breed [ ] Source [ ]
Number: [ ]
Sex: [ ] [ ]
Age: [ ] [ ] [ ] [ ] [ ] [ ]
Height: [ ] [ ] [ ] [ ] [ ]
Height: [ ] [ ] [ ]
Occupation (if appropriate): [ ]
Health Status of Subjects: [ ]
Total Number of Exposures Received: [ ]
  
```

Exposure Group [] of [] of Design []

Note that to the right of this heading and the subsequent fields is a statement "Group [] of [] of Design []." These fields will be filled in by the system which usually begins with exposure group 1 of the total number of groups. The system derives information about the total number of subject groups and exposures from the responses given in the Design screen.

The designation for the first group (they are assigned sequential numbers) comes up automatically. Repetitive use of "return" will move you through the screen.

The screen comes up with the cursor on the "Species" field where the common name of the animal used can be entered. Another "return" places the cursor in the "Breed" field.

Source

"Source" is meant to be used to identify where the animals came from, i.e., the firm which raised them or the agent from whom they were purchased.

Number

"Number" refers to the number of animals in the group.

Sex

Figure 4.2 illustrates the suggested abbreviations for "Sex."

Figure 4.2
Suggested
abbreviations
for "Sex"



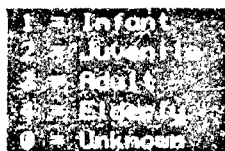
The program converts lower case letters to upper case so there is no need to use the shift key. There are four spaces in the field so it is possible to use some combinations. If all four spaces are filled, the cursor jumps to the next field.

Age

Animal age can be represented in any units using numbers in the first field and units of time in the second. When the cursor is in the second field a note at the bottom of the screen requests that the units be entered. If the age(s) are not given in the report type "UNK" in the space provided. You will still be required to enter a value for "Units."

Finally, enter the age category by selecting the appropriate number from the pop-up list which appears next (Figure 4.3)

Figure 4.3 Age
Category Pop-
Up List



Weight

Subject weights may be entered in any form but they are converted by the program to metric units (kilograms). The first field is for a number and the second for the units (as indicated by the message at the bottom of the screen when the cursor is in the second field). In the event that the subject weight s are not given, enter "UNK" in the space provided for a number. The program still requires that you enter a value for units.

The program also requests that you provide the weight range of the subjects. Select a range from the pop-up list (Figure 4.4).

Figure 4.4
Weight Range
List

Enter letter for weight range			
00 = None	U = Unk	M = Multi-range	
01 = < 1 kg	< 2 lb	06 = 26 - 50 kg	> 55-110 lb
02 = 1 - 2 kg	< 2-4 lb	07 = 51 - 100 kg	> 110-220 lb
03 = 3 - 5 kg	< 4-11 lb	08 = 101 - 200 kg	> 220-440 lb
04 = 6 - 10 kg	< 11-22 lb	09 = 201 - 500 kg	> 440-1100 lb
05 = 11 - 25 kg	< 22-55 lb	10 = 501 - 1000 kg	> 1120-2200 lb

Height

As for "Age" and "Weight," the first field should be a number and the second a unit of measure. Suggested abbreviations are indicated on screen.

Occupation

Papers involving people will often state their occupation(s). There are twenty spaces available for this data entry.

Health Status of Subjects

If this is not reported in the publication, leave the space blank, or indicate that no information is available. If it is, try to indicate the status in the space provided or type a more lengthy statement in the comment section and indicate in this field that there are comments. (THE COMMENT SECTION IS NOT YET READY FOR USE).

5

Exposure Regimen Data Entry

EXPOSURE REGIMEN DATA SCREEN

As with the *SUBJECT GROUP DATA SCREEN*, you can identify which group you are working with by looking at the description under the "Citation No." which tells you how many regimens there are (based on what you typed in previously) and which one you are currently describing. The screen example in Figure 5.1 indicates that data can be entered for the first of 3 total regimens for the first design that was described.

As before, fill in the appropriate data by selecting from the options available when the cursor is in each field. You do not need to fill in every field, only those for which there is an appropriate response defined in the report. For example, if you indicate that there was only one exposure, then you need not fill in the field "Interval." Another option is to fill that field with the word "once."

Figure 5.1
EXPOSURE
REGIMEN
DATA SCREEN

EXPOSURE REGIMEN DATA SCREEN	
Citation No.: [000217-0100-00100-1989]	[]
Regimen No.: [1] of [3] regimens in Study design [1]	[1]
Purpose for Exposure: []	
Agent: []	TOX = Toxic TRT = Treat CTL = Control OTH = Other NCH = None UNK = Unknown
Dose: [] []	
Formulation: [] []	
Route: [] []	
Interval: []	
Duration: []	
Administration Method: []	
Scheduled Evaluation Time: []	

There is no set format for filling in these spaces so try to make the information as descriptive as possible. Filling in all spaces in the field causes the cursor to roll over to the next one. If you do not fill in all spaces in a field you must hit "return" to move to the next field.

Purpose for Exposure

Select one of the potential responses for this field from the pop-up menu on the right side of the screen by typing the appropriate abbreviation in the space provided.

Figure 5.2
Potential
responses
when cursor is
in the

TOX = Toxic
TRT = Treat
CNL = Control
OTH = Other
NON = None
UNK = Unknown

"Purpose for Exposure" field

Agent

There should be sufficient space for you to succinctly define the agent described in the article you are abstracting.

Dose

There are two fields available. One is for providing the quantity (amount), while the other is for the units of measure.

Formulation

The pop-up list to the right of the screen, which is reproduced below, presents the categories appropriate for this field. Type one of the the numbers in the "Formulation" field. You need to type the leading zero.

Figure 5.3
Potential
responses
when cursor is
in the
"Formulation"
field

01 = Solid
02 = Slow-rel
03 = Semisol
04 = Liquid
05 = Spray
06 = Gas
07 = Concent
08 = Feed
09 = Bait
00 = Unk

Route

A pop-up list with selections appropriate for this field appears on the right side of the screen. The possibilities, which are reproduced below, should be sufficient to account for most exposures.

Figure 5.4
Potential
responses
when cursor is
in the "Route"
field

PD = Oral
SK = Dermal
IH = Inhaled
IU = IU Tail
IJ = IJT Inj
IR = IR Inj
SQ = SQ Inj
OC = OC Inj
BT = BT Inj
UK = Unknown

Interval

How often was the agent administered? If it was only once, then you can leave this field blank (hit "return"). If more than once, give the quantity and units of time. An abbreviation which can be useful is "q" for the latin "*quaque*" which means "every." For example, "q4 hr" means every four hours.

If there were multiple administrations and the intervals between treatments were variable, there will not be enough space to list them all. In order to accommodate this specific need, use the "Comment" section.

Duration

In instances where the agent was administered over time, indicate the duration of administration in this field. It does not matter what the route might have been. Some agents are "Comment" section if there were several evaluation times and/or multiple parameters evaluated at different times.

When you fill in the last field, and assuming there are multiple regimens, the next regimen screen is brought up with the cursor on the "Citation No." field. Hit "return" to fill it in. Once again, the up and down arrow (cursor) keys enable you to move between screens, which in this case are regimen descriptions.

When the regimen screen(s) is/are completed for one design, the *STUDY DESIGN DATA SCREEN* comes up and the cycle begins again for each design. Please note that "return" will fill in the "Citation No." field. Hit "return" when the cursor moves to the "Group" field.

When all of the design, subject and regimen screens are complete, you can establish the proper links between them, which constitutes an "Exposure Group." This means placing them within the proper relationships so that, for example, the design for the rabbit portion of the study is properly related to the rabbit subject group and exposure regimen. The "Links" screen is next.

6

Exposure Group Creation

EXPOSURE GROUP LINK ENTRY SCREEN

Overview

The EXPOSURE GROUP LINK ENTRY SCREEN provides a means of storing the associations between designs, subject groups and exposure regimens with their respective results. This screen allows the user to manually define the associations, which then constitute an "Exposure Group." This process creates and stores a derived number for the process along with brief descriptions of the design, subject group and exposure regimen for each "Exposure Group."

Figure 6.1
EXPOSURE
GROUP LINK
ENTRY
SCREEN

```

Use CNTL-P to show Previous page, CNTL-N to show Next page
EXPOSURE GROUP LINK ENTRY SCREEN
Citation Num: [00217-0100-00100-1989] [ ]
Exposure Group: [ ] [ ] [ ] [ ] ExpoGrp [ ] of [ ]
Dsgn: [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ]
Subj: [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ]
Expo: [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ]

1 =3 GRP, 3 EXP, V CNTL
2 =2 GRP, 2 EXP, V CNTL
Design Number
  
```

Design Designation

The "Citation No." can be filled in using "return." "Exposure Group" is not asking you to arbitrarily assign a number or letter for an exposure group. Rather, the first field is for indicating the design for which you are setting up links (see the arrow in the first field after "Exposure Group" in Figure 6.1 above). The choices are given in the lower portion of the screen; use the numbers to the left of the "=" signs, (see the "Dsgn," "Subj," and "Expo" abbreviations below the words "Exposure Group" in Figure 6.1, above). Entering a valid design number (followed by "return") will cause the conditions you entered earlier for that design to pop up (in abbreviated form) next to "Dsgn." Also note that as they are entered, an abbreviated form of each subject description appears mid-screen.

The program keeps track of each association formed and you can identify them by using the "ExpoGrp [] of []" indicators in the upper right of the screen.

Subject Designation

Figure 6.2
EXPOSURE
GROUP LINK
ENTRY
SCREEN with
cursor in the
"Subject
Group" link
field.

Use CNTL-P to show Previous page, CNTL-N to show Next page
EXPOSURE GROUP LINK ENTRY SCREEN

Citation Num: [00217-0100-00100-1980] []
Exposure Group: [100] [01] [00] ExpoGrp [1] of [2]
Dsgn: [3] GRP [3] Exp: CNTL [] 811
Subj: []
Expo: []

Cursor in Subject Group Field

1 -50 RAT, Age: 30 D, Wt: 0.06 KG, Sex: M, 1 EXP
2 -50 RAT, Age: 30 D, Wt: 0.06 KG, Sex: M, 1 EXP
3 -50 RAT, Age: 30 D, Wt: 0.06 KG, Sex: M, 1 EXP

Subject Group Number

After the "Dsgn" number is entered, the cursor moves to the next field where the letter for the subject portion of the link can be entered (see Figure 6.2). Completing the second field of "Exposure Group" causes an abbreviated summary of the subject group description to appear to the right of "Subj:."

Exposure Group Designation

Once again, the choices of regimens described previously are now presented in the middle of the screen, and the cursor is in the "regimen" field. To choose a regimen, place the correct regimen number selected from the right of the "=" signs in the third field of "Exposure Group." Completing this field causes the final field in the "Exposure Group" row to show the abbreviations of the previous three fields with the number of the design (D), subject (S) and exposure regimen (E) linked (see Figure 6.3).

```
Use CNTL-P to show Previous page, CNTL-N to show Next page
EXPOSURE GROUP LINK ENTRY SCREEN
Citation Num: [000217-0100-00100-1989] [ ]
Exposure Group: [1][1][1][1][1][1] S1 E1 ExpoGrp [1] of [1]
Dsgn: [3 GRP, 3 EXP, CNTL] [[ 81]]
Subj: [50 RAT, Age: 30 D, Wt: 0.06 KG, Sex: M, 1 EXP] [[ 197]]
Expo: [LEAD ACETATE, 250 MG/KG PO, given x 1 MIN] [[ 150]]

1 = LEAD ACETATE, 250 MG/KG PO, given x 1 MIN
2 = LEAD, 500 MG/KG PO, given x 1 MIN
3 = CARRIER (WATER), 0.005 MG/KG PO, given x 1 MIN

Exposure Regimen Number
```

The cursor is now on the last field of "ExpoGrp [] of []." Now hit "return," clearing each field and finally filling in the citation number and placing the cursor on the first field to the right of "Exposure Group." A total of 9 "returns" are necessary to reach the point where another "link" can be established. The link process can now begin again for the next subject group for the first design. Repeat the steps as described above.

When the first design is complete, and the cursor is on the first field to the right of "Exposure Group," enter 2 for the second design number and repeat the entry steps until all associations are defined. Complete all the associations for each design, exposure group and regimen.

This currently completes the entry process for TKS-MAIN menu option "New." Other segments are being prepared for addition to the system, including "Comments," "Results," and "Discussion" sections.

7

The Add Path from the ABSTRACT Menu

Add

The "Add" option in the ABSTRACT menu (the ABSTRACT menu is reached by selecting AbstractMgt in the TKS-MAIN menu) provides a means for adding to incomplete citation entries. For example, one can add descriptions of "Designs," "Subject Groups," "Exposure Regimens" and establish "Links."

Figure 7.1
ABSTRACT
Menu and
options

```
ABSTRACT:  New Add Find Exit
Add Citation, PaperContent, Keywords, or Notes to Existing Abstract
```

Selecting "Add" brings you to the "SELECT-FILE-BY" menu. From here, one can search for a specific citation via the author-journal-volume number-first page number-and last two digits of the year, or, by giving the Citation No. (described earlier). The author path requests specific information that you must provide in order for the search process to begin.

Completion of the search process will result in finding the desired citation, or a message that the citation does not exist in the database. If a citation is not in the system, you cannot add anything to it and will have to start from "New" in the ABSTRACT menu.

SELECT-FILE-BY Menu Overview

In order to add information to a file, we have to tell the system which file we would like to add it to.

Figure 7.2
SELECT-FILE-
BY Menu and
options

```
SELECT-FILE-BY:  Author-Name Citation-Number Exit
Find by Author Name
```

There are several ways of locating the file of interest. We can search for it by looking for the first author's last name or the citation number.

Author-Name

This option brings up a prompt which asks you for the author's last name, as indicated in the screen below.

Figure 7.3
SELECT-FILE-
BY Author
 path question
 1

Last name of first author >

Enter the last name and hit "return." Now the program prompts you for the volume or chapter number.

Figure 7.4
SELECT-FILE-
BY Author
 path question
 2

Volume Number or Chapter Number >

Next, one is asked for the first page number of the article.

Figure 7.5
SELECT-FILE-
BY Author
 path question
 3

First page number >

Finally, the last two digits of the year are requested.

Figure 7.6
SELECT-FILE-
BY Author
 path question
 4

Last 2 digits of year >

Currently, you must answer all of the questions posed by this path in order to search for a particular citation. In a later version you will be able to search after answering only one or more of the prompts. This will make it easier under some circumstances, but will also pose some problems. For example, searching via the last name alone will often result in finding more than one paper that matches the search criteria. The user will then have to cycle through them to find the desired one.

Citation-Number

Selecting this option prompts you for the specific citation number (e.g., J00217-0028-00189-1962) on which to do the search. Type in the J or B and the following 5 numbers, a hyphen and the next 4 numbers, a hyphen and 5 numbers, and the year, then "return."

Figure 7.7
SELECT-FILE-
BY Citation
Number path

Which citation number? j00217-0100-00100-1989
Select citation by number

The program either finds a match and brings up the "ADD-DATA" menu asking what you would like to add, finds a match and tells you all data has been entered, or doesn't find a match and lets you know that too. Make sure you typed the citation number correctly before trying to enter new citation information (via the "New" option in the "ABSTRACT" menu), if no match was found.

ADD-DATA Menu

Respond to the SELECT-FILE-BY menu prompts and you will come to the "ADD-DATA" menu.

Figure 7.8
ADD-DATA
Menu and
options

ADD-DATA: Citation-Data Paper-Content Keywords-Notes Exit
Add Citation or Author Data

At this point you will have three basic options available: "Citation Data," "Paper Content," and "Keywords-Notes." The most commonly used option in the current system is "Paper-Content," which consists of the "Paper Overview," "Materials and Methods (including Subject Groups, Exposure Regimens and Links)," "Clinical Findings" (Results) and "Discussion." Citation data is usually entered through the "New" path in "AbstractMgt" as indicated above. Since you already completed at least some of the "Citation-Data" section (otherwise there wouldn't have been anything to find!), you will probably want to use one of the other options.

Citation-Data

This selection allows you to add citation data to material that is already in the system. Since one usually begins entry of a new document by entering the citation, you would not ordinarily need to use this option unless the citation had been deleted after it was entered, or the authors were not entered or complete.

ADD-CITATION-DATA Menu

Since citation data is essentially made up of the citation and author information, you can add those two components by selecting one or the other from this menu.

Figure 7.9
ADD-
CITATION-
DATA Menu
and options

```
ADD-CITATION-DATA:  Citation  Authors  Exit
Add Citation Data
```

Citation

Selecting this option brings up the familiar citation screen. Its use is documented in Chapter 1. If information is already present in the citation screen for this document, you cannot change the screen using this pathway. To modify it you must use the "Update" option in the "BROWSE" menu which can be accessed via the "Find" path.

Authors

Selecting this option brings up the familiar *AUTHOR DATA SCREEN* which can be completed.

If there is already information in the author field(s) for the citation of interest, you cannot change the screen using this pathway. It is necessary to use the "Update" option in the "BROWSE" menu accessed via the "Find" path.

Figure 7.10
AUTHOR
DATA SCREEN
from ADD-
CITATION-
DATA path

```
ADD-CITATION-DATA:  Citation  Authors  Exit
```


AUTHOR DATA SCREEN

Citation: [J00217-0100-00100-1989]	Citrfile: [EXAM.100-100.89]
Author:	AuthSig:
[EXAMPLE 0]	[1]
[[
[[
[[

Hit ESC to leave array.

ADD-CONTENT Menu

The "ADD-CONTENT" menu which appears next requires you to select the type of data that will be entered. Available options include: "PaperOverview," "Materials-Methods," "Results," and "Discussion." One can also go directly from here to the "Find" pathway via "FindData" for doing updates or deletions.

Figure 7.11
ADD-
CONTENT
Menu part I

```
ADD-CONTENT: _ PaperOverview Materials-Methods FindData Results ...
Add overview data regarding the paper
```

Note that the "ADD-CONTENT" options are not all represented at the top of the screen. The three periods (. . .) indicate that there are other options after "Results." Use the cursor to move the highlighted option indicator past "Results" or to the left of "PaperOverview." The top of the screen then looks like the representation below. The option string can be viewed as though it were a circular continuum, where one can move in either direction on the circle.

Figure 7.12
ADD-
CONTENT
Menu part II

```
ADD-CONTENT: _ ... Discussion Exit
```

Selecting "Paper-Content" from the "ADD-DATA" menu brings up the "ADD-CONTENT" menu.

PaperOverview

Selecting this option *may* result in the program reminding you that the overview portion has already been entered, and asking if you would like to "update that information." Selecting "y" followed by "return" will allow you to modify that section. Selecting "n" returns you to the "ADD-CONTENT" menu.

If citation information has been entered but not the "Paper Overview," the *PAPER OVERVIEW SCREEN* will appear.

Materials-Methods

The "MATERIALS METHODS" menu which comes up after this option has been selected has options for "Design," "Subjects," "Regimens," and "Links."

Figure 7.13
MATERIALS-
METHODS
Menu

MATERIALS-METHODS: **Design** Subjects Regimens Links Exit
Add a design to the paper information

Design

Select "Design" and as that screen comes up, be sure to note which design is being displayed (see the "Design No [] of []" statement to the right of the file number).

The Design screen is similar to the one seen in the "new" pathway and is discussed in Chapter 3. "Return" causes the screen to come up with the Citation No. and File No. sections filled in. Type "return" until the first empty field is reached and begin filling in the appropriate responses. The possible options are listed as the cursor moves to each new field.

When all the data for that screen has been entered, hit "Esc" and the next design screen will come up as indicated by the different "Design No. []." If the "Citation No." is not displayed, hit "return" and it will appear.

When all the design screens have been completed, hit "Esc," followed by "e" if you are finished. If the subsequent Subject sections have not been completed, the program will bring you to that section to provide the necessary information. The entry process is similar to that described previously for the *SUBJECT GROUP DATA SCREEN* in Chapter 4.

Subjects

This option permits the addition of subject group data via the *SUBJECT GROUP DATA SCREEN*. The process is similar to that for the *SUBJECT GROUP DATA SCREEN* described previously for a new paper in Chapter 4.

Regimens

This option permits the addition of exposure regimen data via the *EXPOSURE REGIMEN DATA SCREEN*. The process is similar to that for the *EXPOSURE REGIMEN DATA SCREEN* described previously for a new paper in Chapter 5.

Links

This option permits the addition of the *EXPOSURE GROUP LINK ENTRY SCREEN*. The process is similar to that for the *EXPOSURE GROUP LINK ENTRY SCREEN* described previously for a new paper in Chapter 6.

When the *LINK* screen comes up, you must hit "return" first and the program will enter the Citation No. and File No. and show the designs available to choose from.

ResultsSelecting "Results" from the "ADD-CONTENT" menu brings up the the "RESULTS" menu with the "Clinical-Findings" option.

Figure 7.14
RESULTS
Menu

RESULTS: **Clinical Findings** Exit

Clinical Findings

Selecting the "Clinical Findings" option in the "Results" menu brings up the **CLINICAL FINDINGS DATA SCREEN**. Refer to Chapter 9, Results, for directions on using this screen.

Figure 7.15
CLINICAL
FINDING DATA
SCREEN

RESULTS: **Clinical Findings** Exit

CLINICAL FINDING DATA SCREEN

Citation Number: [00217-0100-00100-1989] []

Expo Grp: [] []

[] []

[] []

Clinical Finding: Site [] Effect []

[] []

Change	Severity	Units
[] []	[] []	[] []

Freq	Onset	Duration
[] []	[] []	[] []

H

Discussion

This option is not yet available for use.

Keywords-Notes

Selecting "Keywords-Notes" from the "ADD-DATA" menu allows you to add either keywords or notes (comments), depending on what is selected from the next menu.

ADD-KEYWORDS-NOTES Menu Selecting "Keywords-Notes" from the "ADD-DATA" menu brings up the "ADD-KEYWORDS-NOTES" menu.

Figure 7.16
ADD-
KEYWORDS-
NOTES Menu

ADD-KEYWORDS-NOTES: **Keywords** Notes Exit
Add Keyword Entries

Keywords

Select "Keywords" and the keyword screen comes up. Use of this screen is documented in the section titled *KEYWORD DATA SCREEN* in Chapter 1.

Notes

Select "Notes" and the comment screen will come up. *Do not use this option because it is under development.*

8

The Find Path from the ABSTRACT Menu

ABSTRACT: Find

Selecting "Find" in the ABSTRACT menu (the ABSTRACT menu is reached by selecting AbstractMgt in the TKS-MAIN menu as described in Chapter 1), brings you to the FIND-DATA menu. You can pick from the options available.

Figure 8.1
ABSTRACT
Menu with Find
in reverse
video

```
ABSTRACT:  New Add Find Exit
Find Existing Abstract by Citation, PaperContent, Keywords, or Notes
```

FIND-DATA Menu

The FIND-DATA menu (below) allows you to search for citation data, paper content data, and keywords-notes data. In addition, the option "Top-Down" provides the user with the basic CITATION DATA SCREEN which can be used to initiate a search. If the search is successful, the fields for this screen are filled in including the bottom half of the screen where the number of other components associated with this citation are given. In addition, a "TOP-DOWN" menu appears with the data components listed as options. This allows the user to go immediately to the section of interest, e.g., Authors, Keywords, Paper Overview, Design(s), Materials-Methods, Results or Discussion.

Figure 8.2
FIND-DATA
Menu

```
FIND-DATA:  Citation-Data Paper-Content Keywords-Notes Top-Down Exit
Find Citation or Author Data
```

Select one of the options and follow the screen messages.

Citation-Data

This menu provides you with multiple methods of locating a particular citation. One can specify a Citation No., author(s), volume number, etc., or "Query" for all of those. One can also see the citations and associated information in a different format with different capabilities ("Raw-Citation"). After trying to "Find" a portion of an abstract and discovering it isn't in the system, you can use the "Add" option to add the missing component.

Figure 8.3
FIND-
CITATION-
DATA Menu
and Options

FIND-CITATION-DATA: **Citation** Authors Query-all Raw-Citation ...
Find Citation Data

FIND-CITATION-DATA Menu

Citation

Select "Citation" and the familiar "CITATION DATA SCREEN" appears. Enter various parameters (wild card [*] searches are permitted) and hit "Esc" to initiate the search. The fewer the fields used, the less time the search is likely to take, but the less specific the outcome. In general, there won't be more than a few matches even if only one field is used in the search process. An exception might occur if you search for all papers associated with a particular journal using the wild card approach e.g., "J00217*."

Figure 8.4
CITATION
DATA SCREEN
from the FIND-
CITATION-
DATA path

FIND-CITATION-DATA: **Citation** Authors Query-all Raw-Citation ...

CITATION DATA SCREEN

Citation No: [File No: []
Source: []	File Loc.: []	
Volume/Chap: []	Pages: []-[]	Year: []
Title: -		
[]
[]
[]
[]
Journal/Book Title:		
[]
Authors []	Keywords []	
PaperOver []	Designs []	Subjects [] ExpoRegn []

Help is available. Hit Ctrl-W for help.

In the sample screen below, the "Citation No" was used in the search process. Since all Citation No's are unique, one would expect to find only one match as indicated under the title of the journal in the screen below. Note that an additional menu appears after the search, the "BROWSE" menu.

Figure 8.5
BROWSE
Menu on the
CITATION
DATA SCREEN

```

FIND-CITATION-DATA:  Citation Authors Query-all Raw-Citation ...
|BROWSE:  Next Previous First Last Update Delete Query-Again Exit |
|View the next Citation in the list.                               |
|                                                                    |
|Citation No: [J00217-0100-00100-1989- ] File No: [EXAM.100.100.89 1] |
|Source: [J00217] File Loc.: [ ] |
|Volume/Chap: [100] Pages: [100]-[150] Year: [1989] |
|Title: |
| [THIS IS AN EXAMPLE FOR DOCUMENTATION PURPOSES] |
| [ ] |
| [ ] |
| [ ] |
|Journal/Book Title: |
|[TOXICOL APPL PHARMACOL] |
| 1 rows found. |
|Authors [ 1] Keywords [ 2] |
|PaperOver [ 1] Designs [ 2] Subjects [ 5] ExpoRegn [ 5] |
|                                                                    |
|Help is available. Hit Ctrl-W for help. |
    
```

BROWSE Menu Overview

If the citation is found, a "BROWSE" menu appears from which one can choose to: view the "Next" citation if more than one match is found; see the "Previous" citation if the "Next" or "Last" options were used; go to the "Last" citation in the list of more than one match (the citation matches are arranged chronologically in the order in which they were entered into the system); see the "First" citation if you are elsewhere in the list; "Update" (modify or change) an entry; "Delete" the entry shown on-screen (with the option of deleting other portions of the data, e.g., Paper Overview, Design, etc.); "Query-Again" which clears the data fields and allows one to search for another citation; or "Exit" from the program.

Not all of the options are visible at the top of the screen at one time. To see the others, use the right and left (horizontal) arrow keys to move among the selections and see those on the right after the "...." notation. When the first option is highlighted (Next) you can use the left arrow key to see the end of the option list (horizontal wrap around for the BROWSE option list).

The first few BROWSE options as identified below, should require no further explanation.

Next

Previous

First

Last

Update (Citation)

Selecting "Update" places the cursor on the 'Source' field. You can cycle through the data fields by using the "return" key which functions in only one direction, or the left and right arrow keys.

Change the appropriate field(s) and hit "Esc" when you are finished. Wait for the cursor to return to a data field or menu. This procedure writes the updated information to memory.

The "Author" screen comes up next. Hit "Esc" as indicated at the bottom of the screen. The program will ask if you want to update the author list. If you select "n" the author screen is skipped and the keyword list comes up. Selecting "y" places the cursor on the first data field in the author screen. Change it if necessary, or use the arrow or return keys to cycle through the fields. Modify the entries or type in new authors, and then hit "Esc."

The "Keyword" screen appears next, and the same process occurs again. Refer to the earlier section on keywords in the "New" path (Chapter 1) for information on this screen. When you are finished modifying this screen hit "Esc."

This completes the "Update" process for citations. The program returns you to the citation screen with the "BROWSE" menu. Hit "e" to exit from this environment and return to the FIND-CITATION-DATA screen.

Delete

Invoking the "Delete" option from the "FIND-CITATION-DATA->Citation" pathway brings up a menu titled "DEL-JOURNAL-CIT."

Figure 8.5
DELETE
JOURNAL-CIT
Menu of
CITATION
DATA SCREEN

```

FIND-CITATION-DATA:  Citation Authors Query-all Raw-Citation ...
|DELETE-JOURNAL-CIT:  This-Table All-Tables Exit
|Delete just the data in the citation table
|
|Citation No: [J00217-0100-00100-1989] File No: [EXAM:100.100.89]
|Source: [J00217] File Loc.: [ ]
|Volume/Chap: [100] Pages: [100-1]-[150] Year: [1989]
|Title:
|  THIS IS AN EXAMPLE FOR DOCUMENTATION PURPOSES
|  [REDACTED]
|
|Journal/Book Title:
| [TOXICOL APPL PHARMACOL]
| 1 rows found
|Authors [ 1] Keywords [ 2]
|PaperOver [ 1] Designs [ 2] Subjects [ 5] ExpoRega [ 5]
|
Help is available. Hit Ctrl-W for help.
  
```

The options available are "This-Table" which deletes the table indicated on the screen and "All-Tables" which deletes all of the screens associated with that citation (Paper Overview, Design, Subjects, Regimens, Links, Comments, etc.).

Safe-guards are built in to prevent the latter from happening unless you are *sure* that is what you want. The program gives a warning. If you choose "This-Table" the following question is asked:

Deletion
Prompt:

Are you sure you want to delete this entry? (y/n)
Delete just the data in the citation table

If you choose "All-Tables" the program responds with this question:

Delete All
Tables Prompt

Are you sure you want to delete this entry from all tables? (y/n)

If you respond "n," "return," you are brought back to the 'FIND-CITATION-DATA-BROWSE' menu. If you respond "y," "return," the screen sends messages as each table (screen) is deleted. *There is no way to stop this process once it begins!*

FIND-CITATION-DATA MENU (Continued)

Authors

The author screen can be updated indirectly as described above under BROWSE: Update (Citation), or directly using the "FIND-CITATION-DATA" path as described below.

Selecting "Authors" from the "FIND-CITATION-DATA" menu brings up the author screen with the cursor on the citation number field.

Figure 8.7
AUTHOR
DATA SCREEN

```

FIND-CITATION-DATA:  Citation  Authors  Query-all  Raw-Citation  ...

+-----+
| BROWSE:  Next  Previous  First  Last  Update  Delete  ... |
| View the next Author in the list.                               |
|                               AUTHOR DATA SCREEN                |
| Citation: [                               ] Citfile: [         ] |
| Author:                               AuthSig: [         ] |
| [                               ] [         ] |
| [                               ] [         ] |
| [                               ] [         ] |
| [                               ] [         ] |
+-----+
  
```


Enter the citation number and then Esc." The screen comes up with a message in the lower left corner indicating how many matches were found and asks you to hit "Esc" to continue. A Browse menu appears with options similar to those described above under "Citation."

Author and AuthSig

This screen can also be used to identify articles where an author holds a particular place in the author sequence. For example, if you wanted to determine the "CitationNo." associated with a particular paper where Ueno was the last name of the first author, you could select "Authors" in the "FIND-CITATION-DATA" menu, use the "Return" key to move past "Citation" and "Citfile" to the "Author" field, enter "Ueno Y" (or "Ueno Y*" using the wild card in case someone entered only one initial), followed by "Return." Enter "1" in the "AuthSig" field followed by "Esc" to start the search. The program will locate all citations fitting those criteria and you can "BROWSE" through them to locate the particular one of interest and obtain the desired number.

Figure 8.8
Portion of
BROWSE
Menu
associated
with AUTHOR
DATA SCREEN

```

+-----+
| BROWSE: ... Query-Again Exit |
| Leave this menu |
|                                     AUTHOR DATA SCREEN |
| Citation: [000002-0023-00731-1985] Citfile: [HABE.23.731.85] |
| Author:                                     AuthSig: |
| [HABERMEHL GG]                                     | [1] |
| [BUSAM L]                                           | [2] |
| [HEYDEL P]                                           | [3] |
| [MEBS D]                                             | [4] |
+-----+

```

Query-All

This option provides a mechanism to search for citation, authors or keywords and gives a screen showing all of those components if a match is found.

When "Query-all" is chosen the screen below appears with the cursor in the "Citation Number" field. Use the "return" or cursor keys to select other fields. You can also utilize individual items from several of the component parts (fields) to narrow down the number of matches that may be found. For example, you could enter the year of publication, an author name and a keyword, if you cannot remember specifics such as the "Citation No," "Journal/Book Code" and "Pages."

Please note that you cannot do multiple searches *within* a particular field. For example, you cannot search for two "Authors" or two "Keywords" at the same time. The program keeps you from trying because it moves the cursor to another section as soon as you place data in a particular field

Figure 8.9
QUERY-BY
EXAMPLE
DATA SCREEN

FIND-CITATION-DATA: Citation Authors Query-all Raw-Citation ...					
QUERY-BY-EXAMPLE DATA SCREEN					
Citation Number: [File Code: [
Journ/Book Code	Vol	Pages	Year	Location	
[]	[]	[]
Title of Article or Chapter: [
[
[
[
----- Author -----					
[
[
----- Keyword -----					
[
[
Keycode []]]]	
H					

Raw-Citation

This option invokes another program which provides access to data in the TKS System. It is meant to be used by developers of the TKS System and consists of data fields and their abbreviations. It is necessary to be familiar with the screens in the TKS system in order to interpret the abbreviations. One can access the citation data only, from the Raw-Citation option (two different table types which can be seen by using the "Detail" and "Master" options).

Explanation of the various options can be found under the "Ugly-View" section, below.

Data-Add

This option provides a mechanism for adding data citation components if a search via "FIND" is unsuccessful. Selecting it brings the cursor to an "SELECT-FILE-BY" menu from which the appropriate path (Author-Name or Citation-Number) can be selected for identifying the citation. Use of the "SELECT-FILE-BY" menu is described in Chapter 7.

FIND-DATA Menu (Continued)**Paper-Content**

Figure 8.10
FIND-DATA
Menu

```
FIND-DATA: _ Citation-Data Paper-Content Keywords-Notes Top-Down Exit
Find the contents of the paper
```

To find the data components associated with the 'Paper-Content' (PaperOverview, Materials-Methods, Results and Discussion), choose "Paper-Content" from the "FIND-DATA" menu. The "FIND-CONTENT" menu then appears.

FIND-CONTENT Menu

Figure 8.11
Entire FIND-
CONTENT
Menu

```
FIND-CONTENT: _ PaperOverview Materials-Methods Add-Data Results ...
Find overview data regarding the paper
```

```
FIND-CONTENT: _ ... Ugly-View Discussions Exit
```

In addition to the components described above, one can also access the "Add" path and obtain the "Ugly-View" of the data.

PaperOverview

When this option is selected, a replica of the PAPER OVERVIEW SCREEN comes up with the cursor on the "Citation No." field and the statement "Enter search criteria and hit ESC to search." One can search via any of the fields represented on the screen, (use the "return" or cursor keys to move among the fields) but the "Citation No." and "File No." fields will be most commonly used.

Enter the Citation No. for the paper you wish to find and then "Esc." The program will search and indicate how many matches were found, and a "BROWSE" menu will appear (see Figure 8.12, below). The "BROWSE" options are explained under Find-Citation, above. There is no "Query-Again" option in this "BROWSE" menu.

Figure 8.12
Results of a
FIND-
CONTENT-
>PaperOverview
Search

```

FIND-CONTENT:  PaperOverview  Materials-Methods  Add-Data  Results  ...
|BROWSE:  Next Previous First Last Update Delete  ...
|View the next Paper in the list.
|
|Citation Num:  J00217-0100-00100-1989  File No:  EXAM.100.100.89
|          [ 59 ]
|Stated Purpose:  USE AS AN EXAMPLE FOR DOCUMENTATION PURPOSES
|Implied Purpose:  SAME
|Paper class:  [ 1 ] [ 510 ] EXPER-TOXICITY
|Number of Study Designs in Paper:  [ 2 ]
|
| 1 - 3 GRP - 3 EXP - Y CNTL
| 2 - 2 GRP - 2 EXP - Y CNTL
|
| 1 of 1 rows found.
    
```

Materials-Methods

Choosing this option brings up the "MATERIALS-METHODS" menu where one can then choose from the options "Design," "Subjects," "Regimens," and "Links."

MATERIALS-METHODS Menu

The options available with this menu are illustrated in the screen below. Selecting one of the options brings up the unique data screen associated with that particular option. Since this is part of the "Find" path, associated with each screen is a message asking the user to "Enter search criteria and hit ESC to begin search." One can use any field or combination of fields to initiate the search process.

Figure 8.13
MATERIALS-
METHODS
Menu

```

MATERIALS-METHODS:  Design Subjects Regimens Links Exit
Find a design to the paper information
    
```

When a search is successful the program brings up a screen with data, tells you how many rows matching the search criteria were found, and brings up a "BROWSE" menu. Documentation for the "BROWSE" menu can be found in Chapter 7, however, several additional comments should be made.

Find->BROWSE Menu

Update

This option provides a method for altering data that has already been entered. Cycle through the fields, making corrections as necessary, and hit "Esc" when you are finished, as indicated by the on-screen message.

If you are located in a section which has multiple screens such as multiple "Designs," "Subject" groups, "Regimens," etc., you will notice that if you page back and forth between them (using the up and down cursor keys) that it appears that the data you had changed is back in its old form! Please be aware that this is not so. The data has been changed if you had hit "Esc" appropriately. In order to see the newly altered data it is necessary to exit from the current menu and go back to it, doing another "Query" to pull up the same screens.

Please note that some fields require that you *re-enter* data in order to cycle through the entire screen. This is awkward at times since there is a risk of inaccurately entering information. We are considering improving this feature.

Delete

In each case a protective message appears when "Delete" is selected. You are asked "Do you want to delete this <component> (y/n)," with the component being the particular section just found. You must type in the desired letter (y for "yes" and n for "no"). What happens next is somewhat dependent on the component you are trying to delete. The following is an example: Deleting a design gives you the option to delete only the design on screen, or the visible design screen and all of the screens from that point forward (Subjects, Regimens, Links, etc.). The same is true of "Delete" and the other components of paper content; you can either delete the data on that screen alone, or that screen and all screens linked after it.

The screen messages should provide sufficient information to allow you to complete the "Delete" process.

Query-Again

Selecting this option enables you to perform another search immediately. The screen is cleared of data and the cursor is placed on the first field, which is generally "Citation No."

Add-Data

Selecting this option brings up the "SELECT-FILE-BY" menu which provides two methods for locating data, the "Author-Name" and "Citation-Number" paths. The "SELECT-FILE-BY" menu and how to use it is documented in Chapter 7. When the search is successful the "ADD-DATA" menu appears. It is also documented in Chapter 7.

ResultsChoosing "Results" from the "FIND-CONTENT" menu brings up the "RESULTS" menu which is illustrated below. This menu has one option, "ClinicalFindings." Selecting it brings up the *CLINICAL FINDINGS DATA SCREEN*. *This section is not yet ready for use.*

Figure 8.14
RESULTS
Menu from the
FIND-
CONTENT path

```
RESULTS:  Clinical Findings  Exit
Find Findings entered from Study
```

Figure 8.15
CLINICAL
FINDINGS
DATA SCREEN

```
RESULTS:  Clinical Findings  Exit

CLINICAL FINDING DATA SCREEN
Citation Number: [00217-0100-00100-1989] [ ]
Expo Grp: [ ] [ ]
Clinical Finding: Site [ ] Effect [ ]
Change          Severity Units
[ ] [ ] [ ]
Freq           Onset      Duration
[ ] [ ] [ ]
H
```

Ugly-View

This option is used primarily as a developmental tool by the program developers. Its use is documented in Appendix A.

Discussion

This option is not yet implemented. Selecting it results in a message to that effect appearing on-screen.

Keywords-Notes

Selecting this option brings up the "FIND-KEYWORDS-NOTES" menu with the options indicated in the top of Figure 8.16, below.

FIND-KEYWORDS-NOTES Menu

The "Keywords" option brings up the KEYWORD DATA SCREEN and the usual "Enter search criteria and hit ESC to search" message. One may search for all "Keywords"

associated with a particular citation by entering the appropriate "Citation No." or for all papers containing a particular "Keyword." *Please note that you can only search for one "Keyword" at a time!*

If a search is successful, the findings are put on-screen and the typical "BROWSE" menu appears. Use of this menu is documented above, and in Chapter 7.

Figure 8.16
**FIND-KEYWORDS-
NOTES menu**
and KEYWORD
DATA SCREEN

```

FIND-KEYWORDS-NOTES: Keywords Notes Query-all Exit

```

Enter search criteria and hit ESC to search.
KEYWORD DATA SCREEN

Citation: [_]
 Citfile: [_]
 KeyCode: [_] Keyword: [_]

[]	[]	[]
[]	[]	[]
[]	[]	[]
[]	[]	[]
[]	[]	[]
[]	[]	[]
[]	[]	[]
[]	[]	[]
[]	[]	[]

Notes

This option will provide a mechanism to record specific comments about a paper. It is not yet ready for use.

Query-All

Use of this option was documented earlier in this chapter.

Top-Down Choosing "Top-Down" from the "FIND-DATA" menu brings up the CITATION DATA SCREEN with a message asking you to "Enter search criteria and hit ESC to search."

Figure 8.17
**The FIND-
DATA Menu**
with Top-Down
highlighted

```

FIND-DATA: _ Citation-Data Paper-Content Keywords-Notes Top-Down Exit
See all tables for a selected citation

```

Figure 8.18
Selecting Top-Down brings up the CITATION DATA SCREEN

```

FIND-DATA:  Citation-Data  Paper-Content  Keywords-Notes  Top-Down  Exit
+-----+
|                                     CITATION DATA SCREEN                                     |
| Citation No: [ _ ] File No: [ _ ] |
| Source: [ _ ] File Loc.: [ _ ] |
| Volume/Chap: [ _ ] Pages: [ _ ]-[ _ ] Year: [ _ ] |
| Title: |
| [ |
| [ |
| [ |
| [ |
| Journal/Book Title: |
| [ |
| Authors [ _ ] Keywords [ _ ] |
| PaperOver [ _ ] Designs [ _ ] Subjects [ _ ] ExpoRegm [ _ ] |
+-----+
Help is available. Hit Ctrl-W for help.
    
```

One may choose to search using any of the standard fields or combinations of them. The fields in the lower part of the screen cannot be searched.

If a search is successful, the "BROWSE" menu comes up. If there are multiple matches, such as might occur if you search by "Source" or use a wild-card in the "Citation No." or "File No" fields (J00217* or SMIT*), the "BROWSE" menu will help you to move among the selections. If only one match was found, or you come to the desired selection, hit "e" for exit, and the TOP_DOWN menu appears.

The TOP_DOWN menu gives you immediate access to all the data components of a particular paper by just selecting from its list of options (see Figures 8.19 and 8.20). Selecting from the list brings up the associated data screen which should be familiar. When there are several components, such as multiple subject groups, the "BROWSE" menu which appears allows you to move between them.

Figure 8.19
CITATION
DATA SCREEN
with first part
of TOP_DOWN
menu

```

FIND-DATA:  Citation-Data  Paper-Content  Keywords-Notes  Top-Down  Exit
+-----+
|TOP_DOWN:  Citation  Authors  Keywords  PaperOver  Design  ...|
|Find Citation to serve as top|
|                                     CITATION DATA SCREEN|
|Citation No:[                ] File No:[                ]|
|Source:[                ] File Loc.:[                ]|
|Volume/Chap:[    ] Pages:[    ]-[    ] Year:[    ]|
|Title:|
| [                ]|
| [                ]|
| [                ]|
| [                ]|
|Journal/Book Title:|
| [                ]|
|Authors [    ] Keywords [    ]|
|PaperOver [    ] Designs [    ] Subjects [    ] ExpoReqs [    ]|
+-----+
Help is available. Hit Ctrl-W for help.

```

Figure 8.20
CITATION
DATA SCREEN
with second
part of
TOP_DOWN
menu

```

FIND-DATA:  Citation-Data  Paper-Content  Keywords-Notes  Top-Down  Exit
+-----+
|TOP_DOWN:  ...  Subjects  Regimens  Links  Findings  MoreData  Exit|
|Exit this menu|
|                                     CITATION DATA SCREEN|
|Citation No:[                ] File No:[                ]|
|Source:[                ] File Loc.:[                ]|
|Volume/Chap:[    ] Pages:[    ]-[    ] Year:[    ]|
|Title:|
| [                ]|
| [                ]|
| [                ]|
| [                ]|
|Journal/Book Title:|
| [                ]|
|Authors [    ] Keywords [    ]|
|PaperOver [    ] Designs [    ] Subjects [    ] ExpoReqs [    ]|
+-----+
Help is available. Hit Ctrl-W for help.

```

9

Results -> Clinical Findings

CLINICAL FINDING DATA SCREEN

Completing the "Links" in the "New" pathway from the ABSTRACT menu or selecting "Results" from the ADD-CONTENT menu brings up the CLINICAL FINDING DATA SCREEN shown in Figure 9.1.

Figure 9.1
CLINICAL
FINDING DATA
SCREEN

```

Press F7 or CNTL-G to see available Exposure Groups
CLINICAL FINDING DATA SCREEN
Citation Number: [100006-0018-00267-1980] [ ]
Expo Grp: [ ] [ ]
[ ]
Clinical Finding: Type: [ ] Site [ ] Effect [ ]
[ ]
Change      Severity  Units
[ ] [ ] [ ]
Freq      Onset      Duration
[ ] [ ] [ ]
  
```

Results are generally different for each treatment group. Therefore, the first step in entering results, which are also referred to as "Clinical Findings" is to define the particular exposure group whose results you wish to enter. As you might expect, and as the message at the top of the screen (or Figure 9.1) indicates, the program will show you the exposure groups associated with the citation. These were previously defined in the "Link" screen.

Press function key 7 (F7) or the control and G keys (CNTL-G) and a screen similar to that shown in Figure 9.2 will appear.

Figure 9.2
TKSEXGRP
DATA SCHEEN

```

Press F7 or CNTL-G to see available Exposure Groups
Citation
Expo Grp: Total ExpoGrp: [ 5 ] Citation Num: [ J000006-0018-00267-1980 ]
[ ] Exposure Group Code: [ D1.S2.E2 ] [ 21 ]
[ ] Dsgn: [ 2 GRP, 2 EXP, CNTL ]
[ ] Subj: [ 12 RAT, Age: UNK W, Wt: UNK KG, Sex: B, EXP ]
Clinical Expo: [ T-2 IN MOULDY SORGHU, 25 MG, PO, given DAILY x 16 WEEKS ]
[ ] Exposure Group Code: [ D2.S1.E1 ] [ 22 ]
[ ] Dsgn: [ 3 GRP, 3 EXP, CNTL ]
[ ] Subj: [ 6 MONKEY, Age: UNK Y, Wt: 2-3 KG, Sex: B, EXP ]
Change [ ] Expo: [ MILK AND UNCONTAMINA, 0 MG/KG, PO, given DAILY x 15 DAYS ]
[ ] Exposure Group Code: [ D2.S2.E2 ] [ 23 ]
[ ] Dsgn: [ 3 GRP, 3 EXP, CNTL ]
[ ] Subj: [ 4 MONKEY, Age: UNK Y, Wt: 2-3 KG, Sex: B, EXP ]
ExUse T-2 TOXIN FROM MOULD, 12.5 MG/KG, PO, given DAILY x 15 DAYS
  
```

TKSEXGRP DATA SCREEN

This screen, which overlays the *CLINICAL FINDINGS DATA SCREEN* shows how many exposure groups exist for this citation ("ExpoGrp: []" in upper left corner). You may scroll through the groups by using the up or down cursor (arrow) keys or, with some terminals, the return key. There are often no significant findings for control groups so you can skip to a treatment group which has important clinical findings.

In the above example the user has skipped to Exposure Group Code D2.S2.E2 as indicated by the presence of the the cursor under the "D" in the row with a "23" to the far right. When the cursor is in the right place, hit "Esc" and the abbreviated description is placed in the appropriate field as indicated in Figure 9.3.

Figure 9.3
CLINICAL
FINDING DATA
SCREEN with
Expo Grp Field
Filled

```

Press F7 or CNTL-G to see available Exposure Groups
Citation Number: [ J000006-0018-00267-1980 ] CLINICAL FINDING DATA SCREEN
Expo Grp: [ D2.S2.E2 ] [ 23 ]
[ ]
[ ]
Clinical Finding: Type: [ ] Site [ ] Effect [ ]
[ ]
Change Severity Units
[ ] [ ] [ ]
Freq Onset Duration
[ ] [ ] [ ]
  
```

If the user now hits the "return" key, information describing the selected group is displayed as shown in Figure 9.4.

Figure 9.4
CLINICAL
FINDING DATA
SCREEN with
Expo Grp
Description

```

Press F7 or CNTL-G to see available Exposure Groups
CLINICAL FINDING DATA SCREEN
Citation Number: [J00006-0018-00267-1980] [ ]
Expo Grp: [D2-S2-E2] [ ] [23]
[3 GRP, 3 EXP, CNTL]
[4 MONKEY, Age: UNK, Wt: 2-3 KG, Sex: B, EXP]
[T-2 TOXIN FROM MOULD, 18.5 MG/KG, PO, given DAILY x 15 DAYS]
Clinical Finding: Type: [ ] Site [ ] Effect [ ]
[ ]
Change Severity Units
[ ] [ ] [ ]
Freq Onset Duration
[ ] [ ] [ ]
Exposure Group that produced effect
    
```

Type Field of CLINICAL FINDING DATA SCREEN

Another "return" brings up the options for the "Type" field as shown in Figure 9.5.

Figure 9.5
Options for
"Type" field

```

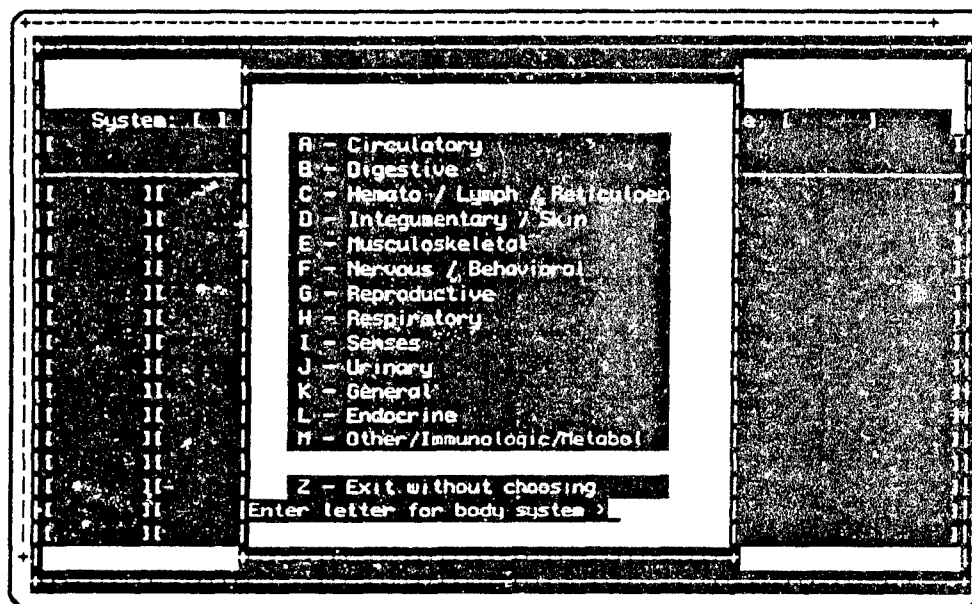
Press F7 or CNTL-G to see available Exposure Groups
CLINICAL FINDING DATA SCREEN
Citation Number: [J00006-0018-00267-1980] [ ]
Expo Grp: [D2-S2-E2] [ ] [23]
[3 GRP, 3 EXP, CNTL]
[4 MONKEY, Age: UNK, Wt: 2-3 KG, Sex: B, EXP]
[T-2 TOXIN FROM MOULD, 18.5 MG/KG, PO, given DAILY x 15 DAYS]
Clinical Finding: Type: [ ] Site [ ] Effect [ ]
[ ]
Change Severity Units
[ ] [ ] [ ]
Freq Onset Duration
[ ] [ ] [ ]
N = Pathology Results
L = Lab/Procedure Results
S = Signs/Disease Finding
    
```

Select from the three choices by typing an "M" for "Pathology Results," "L" for "Laboratory tests" or "Procedure Results," or "S" for "Clinical Signs" or "Disease Findings." Your choice influences what will be seen next.

Pathology Results

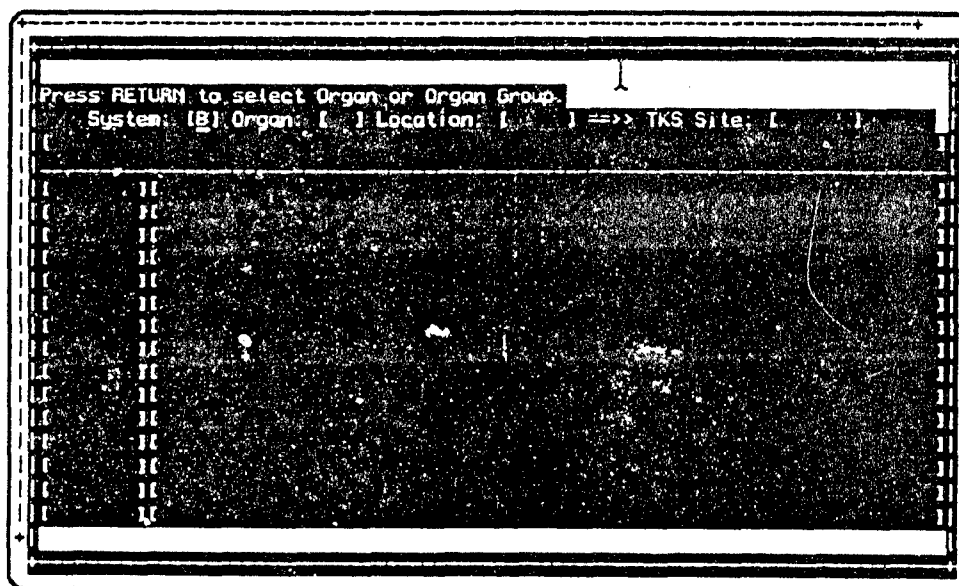
Selecting "M" for "Pathology Results" brings up the SCREEN with a "body system" list overlay.

Figure 9.6
Body System
List



Choose the system related to the clinical finding you wish to describe. In the example given in Figure 9.7, system "B," "DIGESTIVE SYSTEM" was chosen.

Figure 9.7
Select Organ
or Organ
Group Screen



Upon hitting "return" as indicated at the top of the screen the following "Organ" list appears.

Figure 9.8 List Presented when Organ Code "B" is selected

System: [3] Organ: [] Location: [] ==> TKS Site: []

DIGESTIVE

[1]	[1]
[150]	[1]DIGESTIVE SYSTEM IN GENERAL
[151]	[1]MOUTH
[152]	[1]LIP
[153]	[1]TONGUE
[154]	[1]TOOTH, GUM, AND SUPPORTING STRUCTURE OF TOOTH
[155]	[1]SALIVARY GLAND
[156]	[1]LIVER
[157]	[1]GALLBLADDER
[158]	[1]EXTRAHEPATIC BILE DUCT
[159]	[1]EXOCRINE PANCREAS
[15X]	[1]SALIVA
[15V]	[1]BILE AND PANCREATIC FLUID
[160]	[1]PHARYNX, OROPHARYNX AND HYPOPHARYNX
[161]	[1]TONSILS AND ADENOIDS

Use arrow to scroll up and down. Press ESC to select item.

The message at the bottom of the screen tells the user to scroll through the list using the cursor (arrow) keys and then hit "Esc" to make a selection. Please be aware that the list continues beyond the lower limit of the screen!

In our example the user has scrolled to number 59 "EXOCRINE PANCREAS" and hit "Esc," causing the code to be entered in the field after "Organ:."

Figure 9.9 Organ Code Entered

Press RETURN to select Specific Organ Site.

System: [3] Organ: [59] Location: [] ==> TKS Site: []

DIGESTIVE

[1]	[1]
[150]	[1]DIGESTIVE SYSTEM IN GENERAL
[151]	[1]MOUTH
[152]	[1]LIP
[153]	[1]TONGUE
[154]	[1]TOOTH, GUM, AND SUPPORTING STRUCTURE OF TOOTH
[155]	[1]SALIVARY GLAND
[156]	[1]LIVER
[157]	[1]GALLBLADDER
[158]	[1]EXTRAHEPATIC BILE DUCT
[159]	[1]EXOCRINE PANCREAS
[15X]	[1]SALIVA
[15V]	[1]BILE AND PANCREATIC FLUID
[160]	[1]PHARYNX, OROPHARYNX AND HYPOPHARYNX
[161]	[1]TONSILS AND ADENOIDS

Once again, the program leads you through the process, telling the user to hit return to select a specific site (Location), in the message at the top of the screen.

Figure 9.10
Location List
for Code 59

System: [3] Organ: [39] Location: [] ==> TKS Site: []

EXOCRINE PANCREAS

Code	Description
159005	11EXOCRINE PANCREAS, NOS
159010	11PANCREATIC DUCT, NOS
159020	11MUCOUS GLAND OF PANCREATIC DUCT
159030	11DUCT OF WIRSUNG
159040	11DUCT OF SANTORINI
159050	11INTERLOBAR DUCT OF PANCREAS
159060	11INTERLOBULAR DUCT OF PANCREAS
159070	11INTRALOBULAR DUCT OF PANCREAS
159080	11INTERCALATED DUCT OF PANCREAS
159090	11PANCREATIC ACINUS
159100	11HEAD OF PANCREAS
159110	11UNCINATE PROCESS OF PANCREAS
159120	11PANCREATIC INCISURA
159200	11BODY OF PANCREAS

Use arrows to scroll up and down. Press ESC to select item.

Use the "return" key to fill in the "TKS Site" field.

Figure 9.11
TKS Site Field
Filled

Press ESC to main module

System: [3] Organ: [39] Location: [59010] ==> TKS Site: [359010]

PANCREATIC DUCT, NOS

Code	Description
159005	11EXOCRINE PANCREAS, NOS
159010	11PANCREATIC DUCT, NOS
159020	11MUCOUS GLAND OF PANCREATIC DUCT
159030	11DUCT OF WIRSUNG
159040	11DUCT OF SANTORINI
159050	11INTERLOBAR DUCT OF PANCREAS
159060	11INTERLOBULAR DUCT OF PANCREAS
159070	11INTRALOBULAR DUCT OF PANCREAS
159080	11INTERCALATED DUCT OF PANCREAS
159090	11PANCREATIC ACINUS
159100	11HEAD OF PANCREAS
159110	11UNCINATE PROCESS OF PANCREAS
159120	11PANCREATIC INCISURA
159200	11BODY OF PANCREAS

It is now time to locate the specific descriptor for the lesion using the TKS FINDING SYNONYM SCREEN.

Figure 9.12
TKS FINDING
SYNONYM
SCREEN

[illegible]

Enter your search criteria and hit "Esc." In the example below, the user was searching for "inflammation" and used an abbreviation since the system could have it listed as inflammatory or some other similar term. In addition, wild cards were used, both before and after the abbreviation.

Figure 9.13
Search Criteria
In TKS
FINDING
SYNONYM
SCREEN

[illegible]

Figure 9.14 shows the partial listing obtained after the search using *INFLAMM*. Note that if the prefix wild card had not been used the first two items (and some others later on) would not have been found. If the suffix "*" had not been used, *no match would have been obtained* since there is no word with just INFLAMM, even with the wild card prefix. Scroll through the list until you reach the item of interest and hit "Esc" to enter the information in the CLINICAL FINDING DATA SCREEN and open the "change" overlay.

Figure 9.14
List Found
after Search
Using
INFLAMM

Clinical Finding Synonym	TKS FINDING SYNONYM SCREEN
[*INFLAMM*]
[116200]IRADIATION INJURY WITH INFLAMMATION]
[373200]PURPURA, NON-INFLAMMATORY]
[400000]INFLAMMATION, NOS]
[400000]INFLAMMATORY REACTION, NOS]
[400000]INFLAMMATION, ALLERGIC (D-....)]
[400000]INFLAMMATION, IMMUNE COMPLEX ASSOCIATED (F-40500)]
[400000]INFLAMMATION, POSTINFECTIOUS (F-01100)]
[400300]INFLAMMATION, ULCERATIVE, NOS]
[400400]INFLAMMATION, EROSIVE, NOS]
[401600]INFLAMMATION, GIANT CELL]
[402000]INFLAMMATION, DIFFUSE, NOS]
[403000]INFLAMMATION, SEROUS, NOS]
[403000]CATARRHAL INFLAMMATION, NOS]
[403000]TRANSUDATIVE INFLAMMATION, NOS]
[404000]INFLAMMATION, EXUDATIVE, NOS]
Searching....	

The choices for the "Change" field in the TKS FINDING DATA SCREEN are illustrated below. Type the appropriate number and hit "return."

Figure 9.15
Choices for
"Change" field

Citation Number:		TKS FINDING DATA SCREEN	
Expo Grp:	[D2.S2]		
[3] GAP, 3 EXP,			
[5] MONKEY, Age:			
[T-2 TOXIN FROM]			
Clinical Findings:			
[EXOCRINE PANCR]			
[INFLAMMATION]			
Change	S		
[] []	[]		
Freq	Onset		
[]	[]		
Enter number for change seen >			

It now remains for the user to indicate the "Severity" or value of the result along with the units, the "Frequency" of appearance of the path result among the experimental units, the time of "Onset" of the result and its "Duration." Follow the on-screen messages and prompts.

Figure 9.16
Completed
CLINICAL
FINDING DATA
SCREEN

```

CLINICAL FINDING DATA SCREEN
Citation Number: [J00006-0018-00267-1980] [ ]
Expo Grp: [02.S2.E2] [ ] [23]
[3 GRP, 3 EXP, CNTL]
[5 MONKEY, Age: UNK.V, Wt: 2-3 KG, Sex: B, 15 EXP]
[T-2 TOXIN FROM BLOOD: 16.5 mg/KG, PO, given DAILY x 15 DAYS]
Clinical Finding: Type:[ ] Site [359005] Effect [400000]
[EXOCRINE PANCREAS: NOS]
[INFLAMMATION: NOS]
Change Severity Units
[ ] [ABNRM PRES] [MODERATE] [ ]
Freq Onset Duration
[4/4] [16 HOURS] [4 DAYS]
Duration of signs/finding in hours
    
```

Upon completion of these fields, the user can hit "return" and the process will begin anew for the next clinical finding. WHEN YOU ARE FINISHED ENTERING DATA HIT "Esc."

Laboratory/Procedure Results

When "L" is chosen, the sample matrix list is presented (Figure 9.17). Select the type of sample which provided the material for the lab test or procedure by typing the proper letter.

Figure 9.17
Sample Matrix
Overlay

```

Press F7 or CNTL-
CLINICAL FINDING DATA SCREEN
Citation Number:
Expo Grp: [02.S2.E2]
[3 GRP, 3 EXP, CNTL]
[5 MONKEY, Age: UNK.V, Wt: 2-3 KG, Sex: B, 15 EXP]
[T-2 TOXIN FROM BLOOD: 16.5 mg/KG, PO, given DAILY x 15 DAYS]
Clinical Finding:
[ ]
[ ]
Change Severity Units
[ ] [ ] [ ]
Freq Onset Duration
[ ] [ ] [ ]
Enter letter for sample matrix >
A - Blood
B - Plasma
C - Serum
D - Milk
E - Saliva
F - Gastric Content
G - Feces
H - Vomitus
I - Urine
J - CSF
K - Other Matrix
X - Exit w/o Select
    
```

The test category list comes up next (Figure 9.18). Select the appropriate classification.

Figure 9.18
Lab Test
Categories

Clinical Finding	TEST CATEGORY	FINDING SYNONYM SCREEN
	A = Elements/Ions/Inorganics/Acid-Base	
	B = Simple Organics/Carbohydrates	
	C = Proteins/Amino Acids	
	D = Fatty Acids/Lipids/Lipoproteins	
	E = Porphyrins/Bilirubin Copd/Bile Acid	
	F = Purines/Purimadines/Nucleic Acids	
	G = Vitamins	
	H = Hemoglobins	
	I = Enzymes	
	J = Endocrine Substances	
	K = Nervous System Substances	
	L = Immune System Substances	
	M = Hematopoetic Functions	
	Z = Exit without choosing	
	Enter letter for lab test category >	

Now use the TKS FINDING SYNONYM SCREEN to search for the particular parameter of interest.

Figure 9.19
CLINICAL
FINDING
SYNONYM
SCREEN

Clinical Finding Synonym	TKS FINDING SYNONYM SCREEN

In the example shown in Figure 9.20 the user was looking for "calcium."

Hit "Esc" when the cursor is on the correct line and the data will be entered in the "Clinical Finding" field and the descriptors associated with the parameter "Change" will be presented. Choose one from the list (Figure 9.22) and then hit "return."

Figure 9.22
Descriptors for
changes

Citation Number:		ING DATA SCREEN	
Expo Grp: [D2/S3]	<ul style="list-style-type: none"> 0 = NOS 1 = NORMAL 2 = DISORDER 3 = INCREASE 4 = DECREASE 5 = ABSENCE 6 = ABNRM PRESENCE 7 = ABNRM RATIO 	VS	
[6 GRP, 3 EXP]			
[S, NO KEYS] Age:		[A00017]	
[T-2 TOXIN FROM]			
Clinical Finding:			
[SERUM]			
[CALCIUM, NOS]			
Change	S		
[] []	[]		
Freq	Onset		
[] []	[]		
Enter number for change seen >			

Hit "return" again to enter the value in the "Change" field and move to the "Severity" field. Enter the lab value if there is one, or a descriptive term (mild, moderate, severe), hit "return," and enter the "Units," (hit "return" again if you wish to skip this field) followed by another "return" to move to the "Freq" field.

The frequency provides a means to define the proportion affected. As the message at the bottom of the screen indicates, give the number affected / the total exposed for this group.

Next, indicate the time of "Onset" of the change, or the time it was identified.

Figure 9.23
Completed
CLINICAL
FINDING DATA
SCREEN (Lab/
Procedure)

CLINICAL FINDING DATA SCREEN

Citation Number: [J00006-0018-00267-1980] []

Expo Grp: [J2.S2.E2] [] [23]

[3 GAP, 3 EXP, CNTL
5 MONKEY, Age: UNKN, Wt: 2-3 KG, Sex: B, 15 EXP
T-2 TOXIN FROM MOULD, 12.5 MG/KG, PO, given DAILY x 15 DAYS

Clinical Finding: Type: [] Site [TOX50] Effect [700022...]
[SERUM
[CALCIUM, DECREASED LEVEL

Change	Severity	Units
[1] [DECREASE]	[09]	[10G%]

Freq	Onset	Duration
[1/4]	[8 HOURS]	[18 HOURS]

Duration of signs/finding in hours

Finally, the time at which the change was identified is entered in the "Onset" field, and then the length of time the change was present in the "Duration" field. The appearance of a completed screen is shown in Figure 9.23.

When you are finished entering data hit "Esc," to place the data in permanent memory.

Signs/Disease Findings

Selecting "S" from the "Type" list brings up the body system overlay which enables you to choose the system associated with the sign or disease (Figure 9.24).

Figure 9.24
Body System
Overlay

After making your selection, the TKS FINDING SCREEN appears and you can enter your search term, using wild card(s) if necessary. (See the discussions for Pathology Results and Lab/Procedure Results for additional information on these searches)

In the example below, the search term was "**VOMITING*."

Figure 9.25
Search Term
for Signs/
Disease
Findings

Figure 9.26 illustrates the results of that search.

Figure 9.26
Results after
Search on
"VOMITING"

```
|-----|
```

Clinical Finding Synonym	TKS FINDING SYNONYM SCREEN
[*VOMITING*]]

[B01669] VOMITING, NOS]]
[B01671] VOMITING, BILIOUS]]
[B01672] VOMITING, CYCLICAL]]
[B01673] VOMITING, PERIODIC]]
[B01674] VOMITING, PSYCHOGENIC]]
[B01675] VOMITING, HABIT]]
[B01676] VOMITING, PERSISTENT]]
[B01677] VOMITING, PROJECTILE]]
[B01678] NAUSEA AND VOMITING]]
[B01679] NAUSEA, VOMITING AND DIARRHEA]]
[]]]
[]]]
[]]]
[]]]
[]]]
[]]]
Searching....	

```
|-----|
```

Place the cursor on the desired line (B01673 in the above example), and hit "Esc" to enter the information in the "Clinical Finding" field.

Next, select the type of change by entering the number from the list, followed by "return."

Figure 9.27
Type of
Change
Overlay

Citation Number:		ING DATA SCREEN	
Expo Grp:	[02.S2]		
[3 GRP, 3 EXP]			
[4 MONKEY, Age]			
[T-2 TOXIN FROM]			
Clinical Finding:			
[DIGESTIVE]			
[VOMITING, NOS]			
Change	S		
[]	[]		
Freq	Onset		
[]	[]		
Enter number for change seen >			

Now, proceed through the steps to describe the "Severity" of the change as a measured parameter with "Units," or as a subjective grade (e.g., mild, moderate, severe), the "Frequency" of occurrence of the change among experimental units, the time of "Onset,"

and the "Duration" of time the change was observed. A completed screen will appear similar to Figure 9.28.

Figure 9.28
Completed
TKS CLINICAL
FINDING DATA
SCREEN

CLINICAL FINDING DATA SCREEN			
Citation Number: [000006-0018-00267-1990] []			
Expo Grp: [02.S2.E2] [23]			
[3 GRP. 3 EXP. CNTL]			
[5 MONKEY, Age: UNK Y, Ht: 2-3 KG, Sex: B, 15 EXP. 15 DAYS]			
[T-2 TOXIN FROM MOULD, 12.5 MG/KG, PO, given DAILY, 15 DAYS]			
Clinical Finding: Type:[5] Site:[5] Effect:[501678]			
[DIGESTIVE]			
[WHITING, PERIODIC]			
Change	Severity	Units	
[5] [ABNRM PRES]	[MILD]	[]	
Freq	Onset	Duration	
[3/5]	[24 HOURS]	[48 HOURS]	
Duration of signs/finding in hours			

("S" Path)

When the screen is complete hit "return" to bring up a new screen to start the process again for another clinical finding, or hit "Esc" to place the data in system memory.

Modifying Clinical Findings

The *CLINICAL FINDING DATA SCREEN* can be modified using the "BROWSE" menu which is obtained after the screen for a particular citation is located via the "Find" pathway from the "ABSTRACT" menu, or by selecting "FindData" from the "ADD-CONTENT" menu.

Adding Clinical Findings

One can add Clinical Findings to a citation by following the "Add" pathway beginning in the "ABSTRACT" menu, or by selecting "AddData" from the *FIND-CONTENT* menu.

A

Appendix A

FIND-CONTENT: Raw-Citation and Ugly-View

These options are used to obtain another view of the data associated with a citation. It is a different program used primarily as a developmental tool and should not be used by the neophyte. *DO NOT USE THIS OPTION.*

Access to this view will become limited as the database program becomes fully operational.

"Raw-Citation" is the name for this option from the "Citation" pathway, while "Ugly-View" is used for the components from "Taper Content" and beyond. Selecting these options results in the program accessing the *Informix Perform* program which displays a "Perform" menu after about a 30 second delay.

*Figure A.1
Selecting
"Raw-Citation"
or "Ugly-View"
results in this
screen*

```

INFORMIX-SQL Version 2.10.00D
Copyright (C) 1984-1987 Informix Software, Inc.
All Rights Reserved
Software Serial Number RDS*RC59145

```

You will notice that the screen formats are different in this program, providing little explanation for what the data means. Below the menu in the upper right side of the screen is a number and text which will help you keep track of where you are.

The following are the meanings of the abbreviations found in the first window, "Paper Overview."

```

papcitnum = paper citation number
papcitfile = paper citation file
papstatepur = paper statement of purpose
papimpur = paper implied purpose
papaim = paper aim
papnumdsgn = the number of designs in the paper

```

PERFORM Menu

This menu has components which will be familiar to you from other screens, for example, "Next" and "Previous."

Figure A.2
First part of
PERFORM
Menu with
RAW
CITATION
DATA SCREEN

```

PERFORM: Query Next Previous Add Update Remove Table Screen ...
Searches the active database table.                ** 1: citation table**

RAW CITATION DATA SCREEN

citnumb      [
citfile      [
citserial    [
citsource    [
citvol       [ ]
citpage      [ ]
citdate      [ ]
cittitle     [ ]
citlocate    [ ]
    
```

Figure A.2
Second part of
PERFORM
Menu with
RAW
CITATION
DATA SCREEN

```

PERFORM: _ ... Current Master Detail Output Exit
Returns to the INFORMIX-SQL Menu.                ** 1: citation table**

RAW CITATION DATA SCREEN

citnumb      [
citfile      [
citserial    [
citsource    [
citvol       [ ]
citpage      [ ]
citdate      [ ]
cittitle     [ ]
citlocate    [ ]
    
```

Query

This is similar to a search function. It is also an entry process in that it links you with certain data for particular citations. It can be performed at different levels (tables) in the program. For example, if you do a "Query" at the Paper Overview level you can move through the tables in the forward direction for a particular citation to "Study Design," "Subjects,"

"Regimens," "Links," "Clinical Findings," etc. If you do a "Query" starting at the "Design" level, you can't go backward to the "Overview" data table. Selecting "Query" places the cursor on the top data field. "Returns" or the up and down arrow keys can be used to move among the different fields.

Select a field and enter the numbers or words you would like to search for, and hit "Esc" as indicated at the top of the screen. Again, wildcards (*) will prove to be useful as an aid to searching. Did the program find a match? If it did, let's find out how much information has been entered for the paper associated with the "Overview" indicated on the screen.

Add

Update

These options are similar to those described previously under the "Add" and "Find" pathways.

Remove

This option provides a means to delete a row from the active database file.

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Appendix H. Toxin Knowledge System Source Code

Note that the Source Code has its own page number sequencing and table of contents.

Toxin Knowledge System Program Source Code

Version 7.11g5b1a

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Funded by US Army Contract DAMD 17-87-C-7114

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Source Code Overview

The Toxin Knowledge System was developed using software from Informix Software, Inc., 4100 Bohannon Drive, Menlo Park, California, 94025 (415) 926-6300. The database was managed using Informix-SQL™ and the user application was developed using Informix-4GL™. The original development took place on a Sequent™ Balance 8000 minicomputer running Dynix™ (a Unix-based operating system). Eventually the Toxin Knowledge System was ported to an IBM PC/AT platform running MS-DOS 3.3. This development used MS-DOS versions of Informix-SQL™, Informix-4GL™, and Informix-4GL/RDS™. The source code provided is Informix-4GL™ code.

Toxin Knowledge System Source Code

```
#tksglob.4gl
```

```
{Comments:
```

```
TITLE: tksglob.4gl
```

```
Copyright Harold L. Trammel, 1987-1988
```

```
University of Illinois, CVM, IAPIC
```

```
Funded by US Army Contract DAMD-17-C-7114
```

```
}
```

```
DATABASE tkstest
```

```
GLOBALS
```

```
DEFINE
```

```
  #basic table records
```

```
    T_journalst record like journalst.*,
```

```
    T_booklst record like booklst.*,
```

```
    T_citation record like citation.*,
```

```
    T_authors record like authors.*,
```

```
    T_paperover record like paperover.*,
```

```
    T_exporegm record like exporegm.*,
```

```
    T_subjgrp record like subjgrp.*,
```

```
    T_stdydsgn record like stdydsgn.*,
```

```
    T_expogrp record like expogrp.*,
```

```
    T_clinfind record like clinfind.*,
```

```
    T_tkscomment record like tkscomment.*,
```

```
    T_keywords record like keywords.*,
```

```
    T_keylist record like keylist.*,
```

```
    T_tkssite record like tkssite.*,
```

```
    T_morphlst record like morphlst.*,
```

```
    T_morphsynlst record like morphsynlst.*,
```

```
    T_lablst record like lablst.*,
```

```
    T_labsynlst record like labsynlst.*,
```

```
    T_signlst record like signlst.*,
```

```
    T_signsynlst record like signsynlst.*,
```

```
  # array records
```

```
    auth_array ARRAY[10] of RECORD like authors.*,
```

```
    a_array ARRAY[10] of RECORD
```

```
      auth like authors.authname,
```

```
      sig like authors.authsig
```

```
    end record,
```

```
    key_array ARRAY[20] of RECORD like keywords.*,
```

```
    k_array ARRAY[20] of RECORD
```

```
      code like keywords.keycode,
```

```
      keys like keywords.keyword
```

```
    end record,
```

```
    dsgn_array ARRAY[50] of record like stdydsgn.*,
```

```
    expo_array ARRAY[50] of record like exporegm.*,
```

```
    sgrp_array ARRAY[50] of record like subjgrp.*,
```

```
    expg_array ARRAY[50] of record
```

```
      egcnumb like expogrp.egcnumb,
```

```
      egserial integer,
```

```
      egdsgnlabel like expogrp.egdsgnlabel,
```

```
      egsubglabellike expogrp.egsubglabell,
```

```
      egexpolabellike expogrp.egexpolabell,
```

```
      eglink like expogrp.eglink,
```

```
      egtotnum smallint,
```

```
      egdsgndsc like expogrp.egdsgndsc,
```

Toxin Knowledge System Source Code

```
    egdsgn like expogrp.egdsgn,
    egsubgdsc like expogrp.egsubgdsc,
    egsubg like expogrp.egsubg,
    egexpodsc like expogrp.egexpodsc,
    egexpo like expogrp.egexpo
  end record,
  cf_array ARRAY[50] of record like clinfind.*,
  msyn_array ARRAY[50] of record like morphsynlst.*,
  lsyn_array ARRAY[50] of record
    labcode like labsynlst.labcode,
    labsyn like labsynlst.labsyn
  end record,
  ssyn_array ARRAY[50] of record
    signcode like signsynlst.signcode,
    signsyn like signsynlst.signsyn
  end record,
# miscellaneous flags
  jw_flag, bw_flag, cw_flag, awl_flag, kw1_flag, aw_flag    smallint,
  qw_flag, sg_flag, ins_flag, cont_flag smallint,
# window flags
  papwin_flag, dsgnwin_flag, cntlwin_flag, expwin_flag    smallint,
  linkwin_flag, exgppwin_flag, dscwin_flag, comwin_flag    smallint,
  cfwin_flag, cf1win_flag, cf2win_flag, cf3win_flag    smallint,
  morph_flag, lab_flag, sign_flag, syn_flag, site_flag    smallint,
  a265_flag, a270_flag, a260_flag, a260p_flag    smallint,
  a1540_flag, a1940_flag, a875_flag    smallint,
  a1078_flag, a1978_flag    smallint,
# big strings
  query1 char(500),
  select1 char(500),
  select2 char(500),
  bib_entry char(800),
  keywdlst char(420),
  pap_string char(400),
  dsgn_string char(400),
  subj_string char(400),
  expo_string char(400),
  find_string char(400),
# miscellaneous variables
  citnumber like citation.citnumb,
  citfileno like citation.citfile,
  outfile char(30),
  versno char(16),
  quote, beep, answer char(1),
  tmp_cnt, cnt, counter, curr_arr, scr_arr, arr_cnt    smallint,
  curr_exp, exp_cnt, curr_subj, subj_cnt    smallint,
  hold_dsgn integer,
  chosen, x, sw, cw, pw, dw    smallint
END GLOBALS
```

#tksmain.4gl

(Comments:

TITLE: tksmain.4gl

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University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Contains the following functions:

```

empty()
new_abs()
add_abs(t_cit)
find_abs()
select_src()
delete_all(tmp_cit)
)

```

DATABASE tkstest

GLOBALS "tksglob.4gl"

MAIN

define

tmp_cit like citation.citnumb

call versionNum() returning versno

call copyright()

initial setup

let beep = ASCII(7)

let quote = ""

call startlog("tks.errors")

DEFER INTERRUPT

OPTIONS INPUT WRAP,
help file "tkshelp.msg"

DISPLAY "Help is available. Hit Ctrl-W for help." AT 23,1

MENU "TKS-MAIN"

COMMAND "AbstractMgt"

"New Abstract, Add to Abstract, Find Abstracted Data" HELP 10

MENU "ABSTRACT"

COMMAND "New"

"Add new citation and abstract it into database" HELP 20

call new_abs()

COMMAND "Add"

"Add Citation, PaperContent, Keywords, or Notes to Existing Abstract" HELP 21

let tmp_cit = ""

call add_abs(tmp_cit)

COMMAND "Find"

"Find Existing Abstract by Citation, PaperContent, Keywords, or Notes" HELP 22

call find_abs()

COMMAND "Exit" "Leave this MENU" HELP 2

EXIT MENU

END MENU

COMMAND "Vocabulary"

"Access Journal, Book, Keyword, Clinical Finding, or Chemical Vocabulary" HELP 11

MENU "VOCABULARY"

COMMAND "Journals" "Change Journal Listing" HELP 30

CALL j_list()

COMMAND "Books" "Change Book Listing" HELP 30

CALL b_list()

COMMAND "Keywords" "Change Keyword List" HELP 31

call k_list()

Toxin Knowledge System Source Code

```
COMMAND "Signs" "Change Sign or Clinical Finding List" HELP 32
  call s_list()
COMMAND "Chemicals" "Change Chemical List" HELP 33
  CALL empty()
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
COMMAND "Reports" HELP 12
  MENU "REPORTS"
    COMMAND "Journal-Listing"
      "Print current journal listing" HELP 40
      RUN "sacego journalist"
    COMMAND "Exit" HELP 2
    EXIT MENU
  END MENU
COMMAND "Monographs"
  call report_cntl()
COMMAND "Information" HELP 13
  MENU "ADMIN-INFORMATION"
    COMMAND "Copyright-Notice" HELP 1
    call copyright()
    COMMAND "Program-Status" HELP 1
    call showstatus()
    COMMAND "Database-Design" HELP 1
    call data_dict()
    COMMAND "Exit" HELP 2
    EXIT MENU
  END MENU
COMMAND "SQL" "Access ISQL"
  run "pysql"
COMMAND "Exit" HELP 14
  EXIT MENU
END MENU
CLEAR SCREEN
END MAIN
#####
FUNCTION empty()
  ERROR "FUNCTION NOT YET IMPLEMENTED"
  SLEEP 3
  CLEAR SCREEN
END FUNCTION
#####
FUNCTION new_abs()
  define
    tmp_cit like citation.citnumb,
    aim like paperover.papaim
  let tmp_cit = null
  call add_cit(tmp_cit)
  if sw = 1
    then
      return
    else
      let tmp_cit = T_citation.citnumb
      call add_auth(tmp_cit)
      call add_key(tmp_cit)
      call show_fullcit(tmp_cit)
    end if
end if
```

```

call alrt265open()
prompt "Do you want to add content data to system for this paper? (Y/n)"
for char answer
call alrt265close()
if upshift(answer) <> "N"
then
    select * into T_paperover.*
    from paperover
    where papcitnumb = tmp_cit
    if status = NOTFOUND
    then
        call add_paper(tmp_cit)
        if pw = 1
        then
            return
        else
            select papaim into aim from paperover
            where papcitnumb = tmp_cit
            case
            when aim[1,1] = "E"
                call add_exgp(tmp_cit)
                call find_control(tmp_cit)
                exit case
            otherwise
                call empty()
                return
            exit case
            end case
        end if
    else
        Error beep, " Paper Overview data exists for this Paper. Use Find MENU to see
content."
        sleep 3
    end if
end if
END FUNCTION
#####
FUNCTION add_abs(t_cit)
define
    t_cit like citation.citnumb,
    tmp_expo smallint,
    tmp_dsgn smallint,
    totnumdsgn smallint,
    tmp_serial, pge integer,
    tmp_subj smallint
let sw=0
if t_cit is null
then
    call select_src() returning t_cit
    if t_cit is null
    then return
    end if
end if
MENU "ADD-DATA"
COMMAND "Citation-Data"
"Add Citation or Author Data" HELP 60
MENU "ADD-CITATION-DATA"

```

Toxin Knowledge System Source Code

```
COMMAND "Citation"
  "Add Citation Data" HELP 63
  select count(*) into cnt from citation
    where citnumb = t_cit
  if status = NOTFOUND
    then CALL add_cit(t_cit)
    else error "Citation data already entered"
    sleep 2
  end if
COMMAND "Authors"
  "Add Author Entries" HELP 64
  CALL see_auth(t_cit)
  CALL update_auth(t_cit)
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
COMMAND "Paper-Content"
  "Add the contents of the paper" HELP 61
MENU "ADD-CONTENT"
  COMMAND "PaperOverview"
    "Add overview data regarding the paper" HELP 69
    select * into T_paperover.*
      from paperover
      where papcitnumb = t_cit
    if status = NOTFOUND
      then
        call add_paper(t_cit)
      else
        open window alrt1 at 10,3 with 2 rows, 60 columns
          attribute (border, reverse, prompt line first +1)
        display " Paper Overview data exists for this Paper." at 1,1
        prompt "Do you want to update it? (Y/n) > " for answer HELP 23
        close window alrt1
        if upshift(answer) <> "N"
          then
            call papwinopen()
            call disp_paper(t_cit)
            call update_paper(t_cit,
              T_paperover.papserial)
            call papwinclose()
          end if
        end if
      end if
    end if
  COMMAND "Materials-Methods" HELP 70
  MENU "MATERIALS-METHODS"
    COMMAND "Design"
      "Add a design to the paper information" HELP 71
      select papnumdsgn into totnumdsgn
        from paperover
        where papcitnumb = t_cit
      select count(*) into cnt
        from stdydsgn
        where stycitnumb = t_cit
      if totnumdsgn - cnt > 0
        then
          call add_dsgn(t_cit, totnumdsgn, cnt)
          call add_exgp(t_cit)
        else
```

1,1

```

call alrt260plop()
display "Design count is equal to indicated number of designs" at

prompt "Do you want to change PaperOverview? (Y/n) > " for answer
call alrt260p1cl()
if upshift(answer) <> "N"
then
    call papwinopen()
    select * into T_paperover.*
    from paperover
    where papcitnumb = t_cit
    call disp_paper(t_cit)
    call update_paper(t_cit,
        T_paperover.papserial)
    call papwinclose()
end if
end if
COMMAND "Subjects"
"Add subject data for a specific design" HELP 72
open window showdsgn at 2,2 with 21 rows, 75 columns
attribute(border)
#show and select designs
call show_dsgn(t_cit, 0) returning pge
display "Use CNTL-P to show Previous page, CNTL-N to show Next page"

prompt "For which design? " for tmp_dsgn HELP 73
on key (interrupt)
next option "Subjects"
on key (control-P)
call show_dsgn(t_cit, pge-1) returning pge
on key (CONTROL-N)
call show_dsgn(t_cit, pge+1) returning pge
end prompt
select styserial into tmp_serial from stdydsgn
where stycitnumb = t_cit
and stydsgncur = tmp_dsgn
if status = NOTFOUND
then
    error "No designs for that number!"
    sleep 2
    next option "Subjects"
end if
select stynumgrp into tmp_subj from stdydsgn
where stycitnumb = t_cit
and styserial = tmp_serial
close window showdsgn
clear screen
select count(*) into cnt from subjgrp
where sgcitnumb = t_cit
and sgdsgnnum = tmp_serial
call add_sgrp(t_cit, cnt, tmp_subj, tmp_serial)
COMMAND "Regimens"
"Add Exposure Regimen data for a specific design" HELP 74
#show and select designs
call show_dsgn(t_cit, 0) returning pge
display "Use CNTL-P to show Previous page, CNTL-N to show Next page"

```

at 21, 2

Toxin Knowledge System Source Code

```
prompt "For which study design? " for tmp_dsgn HELP 75
  on key(interrupt)
    next option "Regimens"
  on key (control-P)
    call show_dsgn(t_cit, pge-1) returning pge
  on key (CONTROL-N)
    call show_dsgn(t_cit, pge+1) returning pge
  end prompt
select styserial into tmp_serial from stydsgn
  where stycitnumb = t_cit
  and stydsgncur = tmp_dsgn
  if status = NOTFOUND
    then error "No designs for that number!"
    next option "Regimens"
  end if
clear screen
select stynumexp into tmp_expo from stydsgn
  where stycitnumb = t_cit
  and styserial = tmp_serial
select count(*) into cnt from exporegm
  where excitnumb = t_cit
  and exdsgnnum = tmp_serial
call add_expo(t_cit, cnt, tmp_expo, tmp_serial)
COMMAND "Links"
  "Create the Exposure Group links" HELP 77
  call add_exgp(t_cit)
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
COMMAND "FindData"
  "Find previously entered data" HELP 76
  call find_abs()
COMMAND "Results"
  "Enter Findings from Study" HELP 78
  call find_control(t_cit)
COMMAND "Discussion" HELP 79
  call empty()
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
COMMAND "Keywords-Notes" HELP 62
MENU "ADD-KEYWORDS-NOTES"
  COMMAND "Keywords" "Add Keyword Entries" HELP 65
    CALL see_keys(t_cit)
    CALL update_key(t_cit)
  COMMAND "Notes" "Add notes to citation" HELP 66
    call empty()
  COMMAND "Exit" HELP 2
    EXIT MENU
  END MENU
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION flnd_abs()
  let citnumber = ""
```

```

let hold_dsgn = 0
MENU "FIND-DATA"
  COMMAND "Citation-Data"
    "Find Citation or Author Data" HELP 50
  MENU "FIND-CITATION-DATA"
    # Needs mechanism to search for citation data based on
    # authors, journal, etc and select it for adding to the
    # paper data files
    COMMAND "Citation"
      "Find Citation Data" HELP 80
      call find_cit(citnumber)
      call cwinclose()
    COMMAND "Authors"
      "Find Author Entries" HELP 81
      call find_auth(citnumber)
      call auwinclose()
    COMMAND "Query-all"
      "See data for citation, authors, keywords" HELP 82
      call querybib()
    COMMAND "Raw-Citation"
      "See a raw form of the citation, author and keyword data" HELP 83
      run "sperform allcit"
    COMMAND "Data-Add"
      "Add data to system" HELP 84
      let citnumber = ""
      call add_abs(citnumber)
    COMMAND "Exit" HELP 2
    EXIT MENU
  END MENU
COMMAND "Paper-Content"
  "Find the contents of the paper" HELP 51
  MENU "FIND-CONTENT"
    COMMAND "PaperOverview"
      "Find overview data regarding the paper" HELP 90
      call find_paper(citnumber)
      call papwinclose()
    COMMAND "Materials-Methods" HELP 99
    MENU "MATERIALS-METHODS"
      COMMAND "Design"
        "Find a design to the paper information" HELP 91
        call find_dsgn(citnumber)
        call dsgnwinclose()
      COMMAND "Subjects"
        "Find subject data for a specific design" HELP 92
        call find_sgrp(citnumber,hold_dsgn)
        call swinclose()
      COMMAND "Regimens"
        "Find Exposure Regimen data for a specific design" HELP 93
        call find_expo(citnumber,hold_dsgn)
        call expwinclose()
      COMMAND "Links"
        "Find existing Exposure Group link" HELP 94
        call find_exgp(citnumber)
        call linkwinclose()
      COMMAND "Exit" HELP 2
      EXIT MENU
    END MENU
  END MENU

```

Toxin Knowledge System Source Code

```
COMMAND "Add-Data"
  "Add data to system" HELP 95
  let citnumber = ""
  call add_abs(citnumber)
COMMAND "Results" HELP 15
  MENU "RESULTS"
    COMMAND "ClinicalFindings"
      "Find Findings entered from Study" HELP 96
      call find_cfind(citnumber)
      call cf3winclose()
    COMMAND "Exit" HELP 2
    EXIT MENU
  END MENU
COMMAND "Ugly-View"
  "See raw data for all paper content tables" HELP 97
  run "sperform allpaper"
COMMAND "Discussions" HELP 16
  call empty()
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
COMMAND "Keywords-Notes" HELP 52
  MENU "FIND-KEYWORDS-NOTES"
    COMMAND "Keywords"
      "Find Keyword Entries" HELP 53
      call find_key(citnumber)
      call keywinclose()
    COMMAND "Notes"
      "Find notes to citation" HELP 54
      RUN "sperform comment"
    COMMAND "Query-all"
      "See data for citation, authors, keywords" HELP 55
      call querybib()
    COMMAND "Exit" HELP 2
    EXIT MENU
  END MENU
COMMAND "Top-Down"
  "See all tables for a selected citation"
  call top_down() (located in tksquery.4gl)
COMMAND "Exit" HELP 2
  EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION select_src()
  define
    author      char(30),
    volume, vol1, auth1 char(4),
    page2, page1 char(5),
    citdate     char(2),
    t_cit       like citation.citnumb,
    len1, len2  smallint
  Message ""
  let t_cit = ""
  MENU "SELECT-FILE-BY"
    COMMAND "Author-Name" "Find by Author Name" HELP 42
    {
```

This needs better mechanism for:

- situations where an authname might result in similar citfile code
- listing of authors and possible papers similar to show_dsgn()

```

}

message ""
let sw = 0
prompt "Last name of first author > " for author HELP 43
  on key(interrupt)
    let sw=1
  end prompt
  let author = upshift(author)
  let auth1 = author[1,4]
prompt "Volume Number or Chapter Number > " for volume HELP 44
  on key(interrupt)
    let sw=1
  end prompt
prompt "First page number > " for page1 HELP 1
  on key(interrupt)
    let sw=1
  end prompt
prompt "Last 2 digits of year > " for citdate HELP 1
  on key(interrupt)
    let sw=1
  end prompt
let citfileno = auth1 clipped, ".",
  volume clipped, ".",
  page1 clipped, ".",
  citdate
if sw = 1
  then
    next option "Author-Name"
  else
    select citnumb into t_cit
    from citation
    where citfile = citfileno
    if status = notfound
      then
        error beep, "No citation entered for this paper!"
        let t_cit = ""
        message ""
      end if
    EXIT MENU
  end if
COMMAND "Citation-Number"
"Select citation by number" HELP 45
let sw = 0
prompt "Which citation number? " for t_cit HELP 46
  on key(interrupt)
    let sw = 1
  end prompt
let t_cit = upshift(t_cit)
if sw = 1
  then
    next option "Citation-Number"
  else
    select citnumb from citation

```

Toxin Knowledge System Source Code

```
        where citnumb = t_cit
        if status = notfound
            then
                error beep, "No citation entered for this paper!"
                let t_cit = ""
                message ""
            end if
        EXIT MENU
    end if
    COMMAND "Exit" HELP 2
    EXIT MENU
END MENU
return t_cit
END FUNCTION
#####
FUNCTION delete_all(tmp_cit)
    # this is called from delete_cit when all entered papers are to be deleted.
    define
        answer char(1),
        thold, hold smallint,
        tmp_cit like citation.citnumb
    call alrt270open()
    prompt "Are you sure you want to delete this entry from all tables? (y/n) "
    for answer
        call alrt270close()
        if upshift(answer) = "Y"
            then
                select aucitnumb from authors
                    where aucitnumb = tmp_cit
                union
                select keycitnumb from keywords
                    where keycitnumb = tmp_cit
                union
                select papcitnumb from paperover
                    where papcitnumb = tmp_cit
                union
                select stycitnumb from stdydsgn
                    where stycitnumb = tmp_cit
                union
                select sgcitnumb from subjgrp
                    where sgcitnumb = tmp_cit
                union
                select excitnumb from exporegm
                    where excitnumb = tmp_cit
                union
                select egcitnumb from expogrp
                    where egcitnumb = tmp_cit
                union
                select cfcitnumb from clinfind
                    where cfcitnumb = tmp_cit
                union
                select cocitnumb from tkacomment
                    where cocitnumb = tmp_cit
            if status = NOTFOUND
                then
                    delete from citation where citnumb = tmp_cit
                    clear form
```

```

Message "ROW DELETED - no other rows!!"
  sleep 1
  Message ""
else
  delete from citation where citnumb = tmp_cit
  clear form
  call alrt265open()
  message beep,
    "There is information in other tables with this number!"
  sleep 2
  let thold = 0
  select count(*) into hold from authors
    where aucitnumb = tmp_cit
  delete from authors
    where aucitnumb = tmp_cit
  display "" at 2,1
  display " ", hold using "##&", "author rows deleted" at 2,1
  sleep 2
  select count(*) into hold from keywords
    where keycitnumb = tmp_cit
  delete from keywords
    where keycitnumb = tmp_cit
  display "" at 2,1
  display " ", hold using "##&", "keyword rows deleted" at 2,1
  sleep 2
  select count(*) into hold from paperover
    where papcitnumb = tmp_cit
  delete from paperover
    where papcitnumb = tmp_cit
  display "" at 2,1
  display " ", hold using "##&", "paper overview rows deleted" at 2,1
  sleep 2
  select count(*) into hold from stdydsgn
    where stycitnumb = tmp_cit
  delete from stdydsgn
    where stycitnumb = tmp_cit
  display "" at 2,1
  display " ", hold using "##&", "study design rows deleted" at 2,1
  sleep 2
  select count(*) into hold from subjgrp
    where sgcitnumb = tmp_cit
  delete from subjgrp
    where sgcitnumb = tmp_cit
  display "" at 2,1
  display " ", hold using "##&", "subject group rows deleted" at 2,1
  sleep 2
  select count(*) into hold from exporegm
    where excitnumb = tmp_cit
  delete from exporegm
    where excitnumb = tmp_cit
  display "" at 2,1
  display " ", hold using "##&", "exposure regimen rows deleted" at 2,1
  sleep 2
  select count(*) into hold from expogrp
    where egcitnumb = tmp_cit
  delete from expogrp
    where egcitnumb = tmp_cit

```

Toxin Knowledge System Source Code

```
        display "" at 2,1
        display " ", hold using "##&", " exposure group rows deleted" at 2,1
        sleep 2
        select count(*) into hold from clinfind
        where cfcitnumb = tmp_cit
        delete from clinfind
        where cfcitnumb = tmp_cit
        display "" at 2,1
        display " ", hold using "##&", " clinical finding rows deleted" at 2,1
        sleep 2
        select count(*) into hold from tkacomment
        where cocitnumb = tmp_cit
        delete from tkacomment
        where cocitnumb = tmp_cit
        display "" at 2,1
        display " ", hold using "##&", " comment rows deleted" at 2,1
        sleep 2
        call alrt265close()
    end if
else
    clear form
    message "Row NOT deleted"
    sleep 1
    message ""
    return
end if
END FUNCTION
```


Toxin Knowledge System Source Code

#tkpdev.4gl

(TITLE: tkpdev.4gl

Copyright Harold L. Trammel, 1987-1988

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

PURPOSE: to list the status of the developmental TKS

Contains the following functions:

versionNum()

showstatus()

data_dict()

copyright()

)

database tkstest

globals "tksglob.4gl"

#####

FUNCTION versionNum()

{DEVELOPMENT NOTES

1. Version Numbers 10-14-88

TKS Version numbers should indicate the number of major revisions, the number of gamma level modules, the number of beta level module, and the number of alpha modules.

major revisions - changes made to the majority of the modules these changes would reduce affected modules from gamma level to beta level until changes confirmed correct.

gamma level - module has been debugged to a reasonable level and can be used safely by non-programming and testing staff

beta level - module that have high level of development and programmer level debugging.

alpha level - initial development modules, prone to have bugs a' plenty

10-14-88 version number= tks5.9g8b2a

Citation data fully operational

Paper Content partially operational

Monograph Begun

Vocabulary fully operational xc SNOVET into SNOMED

12-25-88 version number tks6.9g8b2a

Help messages added to all modules

1-26-89 version number tks7.5g3b11a

Added serial numbers to all tables, modifications to all modules to provide support of those numbers

4-3-89 version number tks7.11g.5b.1a

Supports serial numbers all the way to finding.

Finding needs almost full revision.

10-6-89 version number tks7.10g.5b.2b

Vocabulary modules significantly revised; clinical finding

}

define

vers char(25)

let vers = "tks7.10g5b2a"

return vers

```

end function
#####
function showstatus()
  open window devwin at 3,4 with 18 rows, 75 columns attribute(border)
  display "STATUS - DEVELOPMENTAL TOXIN KNOWLEDGE SYSTEM" at 2,1
  display "" at 3,1
  display "main gamma"      at 4,3
  display "globals gamma"   at 4,30
  display "citation gamma"   at 6,3
  display "authors gamma"   at 6,30
  display "keywords gamma"  at 6,50
  display "query gamma"     at 8,3
  display "shows gamma"     at 8,30
  display "paperoverview gamma" at 10,3
  display "design beta"      at 10,30
  display "subjgrp beta"    at 10,50
  display "exporegm beta"   at 12,3
  display "expogrp beta"    at 12,30
  display "findings alpha"  at 12,50
  display "vocabulary alpha" at 14,3
  display "monograph beta"  at 14,30
  display "translation gamma" at 16,3
  display "window mgt gamma" at 16,30
  sleep 4
  close window devwin
end function
#####
function data_dlist()
  clear screen
  display "Getting the information ... " at 10,30
  attribute(reverse)
  run "isql lkstest infotks > infotks.out"
  run "less infotks.out"
  display "" at 10,30
end function
#####
function copyright()
  call alrt1540open()
  display " _____ " at 2,2 attribute(reverse)
  display " / | | / / / " at 3,2 attribute(reverse)
  display " | | < < _____ " at 4,2 attribute(reverse)
  display " | | \ \ > " at 5,2 attribute(reverse)
  display " _/ _/ > _____ / " at 6,2 attribute(reverse)
  display " " at 7,2 attribute(reverse)
  display "Toxin Knowledge System ver.",versno clipped at 9,2
  display "Copyright 1988,1989 Harold L. Trammel " at 10,2
  display " University of Illinois " at 11,2
  display " Funded by " at 13,2
  display " US Army Contract DAMD17-C-87-7114 " at 14,2
  sleep 5
  call alrt1540close()
end function

```

Toxin Knowledge System Source Code

#tkswinmg.4gl

(TITLE: tkswinmg.4gl

Copyright Harold L. Trammel, 1987-1988

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Purpose: central file to hold window management functions for entire program

Contains the following functions:

- alrt1940open()
- alrt1940close()
- alrt260open()
- alrt260close()
- alrt270open()
- alrt270close()
- alrt260p1op()
- alrt260p1cl()
- alrt265open()
- alrt265close()
- alrt1540open()
- alrt1540close()
- alrt875open()
- alrt875close()
- qwinopen()
- qwinclose()
- auwinopen()
- auwinclose()
- keywinopen()
- keywinopen()
- cwinopen()
- cwinclose()
- papwinopen()
- papwinopen()
- papwinclose()
- dsgnwinopen()
- dsgnwinopen()
- dsgnwinclose()
- expwinopen()
- expwinopen()
- expwinclose()
- swinopen()
- swinopen()
- swinclose()
- linkwinopen()
- linkwinopen()
- linkwinclose()
- exgpwinopen()
- exgpwinopen()
- exgpwinclose()
- dscwinopen()
- dscwinopen()
- dscwinclose()
- cfwinopen()
- cfwinopen()
- cfwinclose()
- cf1winopen()
- cf1winopen()
- cf1winclose()
- cf2winopen()
- cf2winopen()
- cf2winclose()
- cf3winopen()
- cf3winopen()
- cf3winclose()
- alrt1078open()
- alrt1078open()
- alrt1078close()

```

morphwinopen()
morphwinclose()
sitewinopen()
sitewinclose()
labwinopen()
labwinclose()
signwinopen()
signwinclose()
synwinopen()
synwinclose()
}

database tkstest
globals "tksglob.4gl"

#####
FUNCTION alrt1940open()
if a1940_flag <> 1
  then
    open window alrt1940 at 4,20 with 19 rows, 40 columns
      attribute (border, reverse, prompt line last -1)
    let a1940_flag = 1
  else
    current window is alrt1940
  end if
end function

#####
FUNCTION alrt1940close()
if a1940_flag = 1
  then
    close window alrt1940
    let a1940_flag = 0
  end if
END FUNCTION

#####
FUNCTION alrt260open()
if a260_flag <> 1
  then
    open window alrt260 at 10,10 with 2 rows, 60 columns
      attribute (border,reverse)
    let a260_flag = 1
  else
    current window is alrt260
  end if
end function

#####
FUNCTION alrt260close()
if a260_flag = 1
  then
    close window alrt260
    let a260_flag = 0
  end if
END FUNCTION

```

Toxin Knowledge System Source Code

```
#####  
FUNCTION alrt270open()  
if a270_flag <> 1  
then  
    open window alrt270 at 10,5 with 2 rows, 70 columns  
    attribute (border,reverse)  
    let a270_flag = 1  
else  
    current window is alrt270  
end if  
end function  
  
#####  
FUNCTION alrt270close()  
if a270_flag = 1  
then  
    close window alrt270  
    let a270_flag = 0  
end if  
END FUNCTION  
  
#####  
FUNCTION alrt260p1op()  
if a260p_flag <> 1  
then  
    open window alrt260p1 at 10,10 with 2 rows, 60 columns  
    attribute (border,reverse, prompt line first+1)  
    let a260p_flag = 1  
else  
    current window is alrt260p1  
end if  
end function  
  
#####  
FUNCTION alrt260p1cl()  
if a260p_flag = 1  
then  
    close window alrt260p1  
    let a260p_flag = 0  
end if  
END FUNCTION  
  
#####  
FUNCTION alrt265open()  
if a265_flag <> 1  
then  
    open window alrt265 at 10,7 with 2 rows, 65 columns  
    attribute (border,reverse)  
    let a265_flag = 1  
else  
    current window is alrt265  
end if  
end function  
  
#####  
FUNCTION alrt265close()  
if a265_flag = 1
```

```

    then
        close window alrt265
        let a265_flag = 0
    end if
END FUNCTION

#####
FUNCTION alrt1540open()
if a1540_flag <> 1
    then
        open window alrt1540 at 5,20 with 15 rows, 40 columns
        attribute (border)
        let a1540_flag = 1
    else
        current window is alrt1540
    end if
end function

#####
FUNCTION alrt1540close()
if a1540_flag = 1
    then
        close window alrt1540
        let a1540_flag = 0
    end if
END FUNCTION

#####
FUNCTION alrt875open()
if a875_flag <> 1
    then
        open window alrt875 at 5,2 with 8 rows, 75 columns
        attribute (border)
        let a875_flag = 1
    else
        current window is alrt875
    end if
end function

#####
FUNCTION alrt875close()
if a875_flag = 1
    then
        close window alrt875
        let a875_flag = 0
    end if
END FUNCTION

#####
FUNCTION qwinopen()
display "" at 2,2
if qw_flag <> 1
    then
        open window querywin at 2,2 with form "querybib"
        attribute(border)
        let qw_flag = 1
        display "" at 1,1

```

Toxin Knowledge System Source Code

```
        display "" at 2,2
    else
        current window is querywin
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

```
#####
FUNCTION qwinclose()
display "" at 2,2
if qw_flag = 1
    then
        close window querywin
        let qw_flag = 0
    end if
end FUNCTION
```

```
#####
FUNCTION auwinopen()
display "" at 2,2

if aw1_flag <> 1
    then
        OPEN WINDOW auwin1 at 12,3 WITH FORM "tksauth"
        ATTRIBUTE (border)
        let aw1_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is auwin1
        display "" at 1,1
        display "" at 2,2
    end if
end function
```

```
#####
FUNCTION auwinclose()

display "" at 2,2
if aw1_flag = 1
    then close window auwin1
        let aw1_flag = 0
    end if
end function
```

```
#####
FUNCTION keywinclose()
display "" at 2,2
    if kw1_flag = 1
        then
            close window kwin1
            let kw1_flag = 0
        end if
    end function
```

#####

FUNCTION keywinopen()

display "" at 2,2

if kw1_flag <> 1

then

OPEN WINDOW kewin1 at 4,29 WITH 18 rows, 50 columns

ATTRIBUTE (border)

open form k_wrds from "tkskey"

display form k_wrds

let kw1_flag = 1

display "" at 1,1

display "" at 2,2

else

current window is kewin1

display "" at 1,1

display "" at 2,2

display "" at 16,2

end if

end function

#####

FUNCTION cwinopen()

display "" at 2,2

if cw_flag <> 1

then

OPEN WINDOW cit1 at 2,2 WITH FORM "tkscit" ATTRIBUTE (BORDER)

let cw_flag = 1

display "" at 1,1

display "" at 2,2

else

current window is cit1

display "" at 1,1

display "" at 2,2

end if

end function

#####

FUNCTION cwinclose()

display "" at 2,2

if cw_flag = 1

then

close window cit1

let cw_flag = 0

end if

end function

#####

FUNCTION papwinopen()

display "" at 2,2

if papwin_flag <> 1

then

open window paperwin at 2,2 with form "tkspaper"

attribute(border)

Toxin Knowledge System Source Code

```
        let papwin_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is paperwin
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

```
#####
FUNCTION papwinclose()
display "" at 2,2
if papwin_flag = 1
    then
        close window paperwin
        let papwin_flag = 0
    end if
end FUNCTION
```

```
#####
FUNCTION dsgnwinopen()
display "" at 2,2
if dsgnwin_flag <> 1
    then
        open window dsgnwin at 2,2 with form "tkdsgn"
        attribute(border)
        let dsgnwin_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is dsgnwin
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

```
#####
FUNCTION dsgnwinclose()
display "" at 2,2
if dsgnwin_flag = 1
    then
        close window dsgnwin
        let dsgnwin_flag = 0
    end if
end FUNCTION
```

```
#####
FUNCTION expwinopen()
display "" at 2,2
if expwin_flag <> 1
    then
        open window expwin at 2,2 with form "tksexpo"
```

```

        attribute(border)
        let expwin_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is expwin
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION

```

```

#####
FUNCTION expwinclose()
display "" at 2,2
if expwin_flag = 1
    then
        close window expwin
        let expwin_flag = 0
    end if
end FUNCTION

```

```

#####
FUNCTION swinopen()
display "" at 2,2
if sg_flag <> 1
    then
        OPEN WINDOW sgrp1 at 2,2 WITH FORM "tkssubj" ATTRIBUTE (BORDER)
        let sg_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is sgrp1
        display "" at 1,1
        display "" at 2,2
    end if
end function

```

```

#####
FUNCTION swinclose()
display "" at 2,2
if sg_flag <> 1
    then
        close window sgrp1
        let sg_flag = 0
    end if
end function

```

```

#####
FUNCTION linkwinopen()
display "" at 2,2
if linkwin_flag <> 1
    then
        open window linkwin at 2,2 with form "tkseg1"

```

Toxin Knowledge System Source Code

```
        attribute(border)
        let linkwin_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is linkwin
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

#####

FUNCTION linkwinclose()

```
display "" at 2,2
if linkwin_flag = 1
    then
        close window linkwin
        let linkwin_flag = 0
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

#####

FUNCTION exgpwinopen()

```
display "" at 2,2
if exgpwin_flag <> 1
    then
        open window exgpwin at 5,3 with form "tkseg2"
        attribute(border)
        let exgpwin_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is exgpwin
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

#####

FUNCTION exgpwinclose()

```
display "" at 2,2
if exgpwin_flag = 1
    then
        close window exgpwin
        let exgpwin_flag = 0
    end if
end FUNCTION
```

#####

FUNCTION dscwinopen()

```
display "" at 2,2
if dscwin_flag <> 1
```

```

then
  open window dscwin at 10,3 with 10 rows, 65 columns
  attribute(border)
  let dscwin_flag = 1
  display "" at 1,1
  display "" at 2,2
else
  current window is dscwin
  display "" at 1,1
  display "" at 2,2
end if
end FUNCTION

```

```

#####
FUNCTION dscwinclose()
display "" at 2,2
if dscwin_flag = 1
  then
    close window dscwin
    let dscwin_flag = 0
  end if
end FUNCTION

```

```

#####
FUNCTION cfwinopen()
display "" at 2,2
if cfwin_flag <> 1
  then
    open window cfwin1 at 2,2 with form "tkscf"
    attribute(border)
    let cfwin_flag = 1
    display "" at 1,1
    display "" at 2,2
  else
    current window is cfwin1
    display "" at 1,1
    display "" at 2,2
  end if
end FUNCTION

```

```

#####
FUNCTION cfwinclose()
display "" at 2,2
if cfwin_flag = 1
  then
    close window cfwin1
    let cfwin_flag = 0
  end if
END FUNCTION

```

```

#####
FUNCTION cf1winopen()
display "" at 2,2
if cf1win_flag <> 1

```

Toxin Knowledge System Source Code

```
    then
        open window cfind1 at 2,2 with form "tkscf1"
        attribute(border)
        let cf1win_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is cfind1
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

```
#####
FUNCTION cf1winclose()
display "" at 2,2
if cf1win_flag = 1
    then
        close window cfind1
        let cf1win_flag = 0
    end if
END FUNCTION
```

```
#####
FUNCTION cf2winopen()
display "" at 2,2
if cf2win_flag <> 1
    then
        open window cfind2 at 2,2 with form "tkscf2"
        attribute(border)
        let cf2win_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is cfind2
        display "" at 1,1
        display "" at 2,2
    end if
end FUNCTION
```

```
#####
FUNCTION cf2winclose()
display "" at 2,2
if cf2win_flag = 1
    then
        close window cfind2
        let cf2win_flag = 0
    end if
END FUNCTION
```

```
#####
FUNCTION cf3winopen()
display "" at 2,2
```

```

if cf3win_flag <> 1
  then
    open window cfind3 at 2,2 with form "tkscf3"
    attribute(border)
    let cf3win_flag = 1
    display "" at 1,1
    display "" at 2,2
  else
    current window is cfind3
    display "" at 1,1
    display "" at 2,2
end if
end FUNCTION

```

```

#####

```

```

FUNCTION cf3winclose()

```

```

display "" at 2,2

```

```

if cf3win_flag = 1

```

```

  then

```

```

    close window cfind3

```

```

    let cf3win_flag = 0

```

```

end if

```

```

END FUNCTION

```

```

#####

```

```

FUNCTION alrt1978open()

```

```

if a1978_flag <> 1

```

```

  then

```

```

    open window alrt1978 at 2,2 with 19 rows, 78 columns

```

```

    attribute (border)

```

```

    let a1978_flag = 1

```

```

  else

```

```

    current window is alrt1978

```

```

end if

```

```

end function

```

```

#####

```

```

FUNCTION alrt1978close()

```

```

if a1978_flag = 1 then

```

```

  close window alrt1978

```

```

  let a1978_flag = 0

```

```

end if

```

```

END FUNCTION

```

```

#####

```

```

FUNCTION alrt1078open()

```

```

if a1078_flag <> 1

```

```

  then

```

```

    open window alrt1078 at 12,2 with 10 rows, 78 columns

```

```

    attribute (border)

```

```

    let a1078_flag = 1

```

```

  else

```

```

    current window is alrt1078

```

```

end if

```

Toxin Knowledge System Source Code

end function

#####

FUNCTION alrt1078close()

if a1078_flag = 1 then
 close window alrt1078
 let a1078_flag = 0

end if

END FUNCTION

#####

FUNCTION morphwinopen()

display "" at 2,2

if morph_flag <> 1

then

 OPEN WINDOW morph at 2,2 WITH FORM "vocmorph" ATTRIBUTE (BORDER)

 let morph_flag = 1

 display "" at 1,1

 display "" at 2,2

else

 current window is morph

 display "" at 1,1

 display "" at 2,2

end if

end function

#####

FUNCTION morphwinclose()

display "" at 2,2

if morph_flag = 1

then

 close window morph

 let morph_flag = 0

end if

end function

#####

FUNCTION sitewinopen()

display "" at 2,2

if site_flag <> 1

then

 OPEN WINDOW site at 2,2 WITH FORM "vocsite" ATTRIBUTE (BORDER)

 let site_flag = 1

 display "" at 1,1

 display "" at 2,2

else

 current window is site

 display "" at 1,1

 display "" at 2,2

end if

end function

#####

FUNCTION sitewinclose()

display "" at 2,2

```

    if site_flag = 1
    then
        close window site
        let site_flag = 0
    end if
end function

#####
FUNCTION labwinopen()
display "" at 2,2
    if lab_flag <> 1
    then
        OPEN WINDOW lab at 2,2 WITH FORM "voclab" ATTRIBUTE (BORDER)
        let lab_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is lab
        display "" at 1,1
        display "" at 2,2
    end if
end function

#####
FUNCTION labwinclose()
display "" at 2,2
    if lab_flag = 1
    then
        close window lab
        let lab_flag = 0
    end if
end function

#####
FUNCTION signwinopen()
display "" at 2,2
    if sign_flag <> 1
    then
        OPEN WINDOW sign at 2,2 WITH FORM "vocsign" ATTRIBUTE (BORDER)
        let sign_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is sign
        display "" at 1,1
        display "" at 2,2
    end if
end function

#####
FUNCTION signwinclose()
display "" at 2,2
    if sign_flag = 1
    then
        close window sign

```


Toxin Knowledge System Source Code

```
        let sign_flag = 0
        end if
    end function

#####
FUNCTION synwinopen()
display "" at 2,2
    if syn_flag <> 1
    then
        OPEN WINDOW syn at 2,2 WITH FORM "tkssynls" ATTRIBUTE (BORDER)
        let syn_flag = 1
        display "" at 1,1
        display "" at 2,2
    else
        current window is syn
        display "" at 1,1
        display "" at 2,2
    end if
end function

#####
FUNCTION synwinclose()
display "" at 2,2
    if syn_flag = 1
    then
        close window syn
        let syn_flag = 0
    end if
end function
```

#tkscit.4gl

{TITLE: tkscit.4gl

Copyright Harold L. Trammel, 1987-1988

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Contains the following FUNCTIONS:

```

    add_cit(argcit)
    find_cit(t_cit)
    view_cit()
    update_cit(tmp_citserial)
    delete_cit(tmp_citserial)
    distitle()
    see_journ()
    see_book()
    get_auth1()
    citnumb_exists(c_num)
    citfile_exists(c_file)
    exist_citnumb(c_cit)
    exist_citfile(c_cit)
}

```

DATABASE tkstest

GLOBALS "tksglob.4gl"

#####

FUNCTION add_cit(argcit)

DEFINE

```

    ctitle1, ctitle2, ctitle3, ctitle4 char(63),
    cpage1, cpage2, cpage3, tmp_page char(5),
    cvol, thisyear char(4),
    len1, len2, len3, x, y smallint,
    tmp_auth like authors.authname,
    tmpname char(60),
    tmp_add char(2),
    argcit like citation.citnumb,
    argfile like citation.citfile,
    cc integer,
    auth1 like authors.authname

```

#initial screen setup

call cwinopen()

CLEAR FORM

display "" at 15,2

let sw = 0

display "0" to authors

display "0" to keywords

display "0" to paperover

display "0" to designs

display "0" to subjects

display "0" to exposures

call get_auth1() returning auth1

options input wrap,

help file "tkshelp.msg",

help key CONTROL-n

INPUT

T_citation.citsource,

T_citation.citlocate,

T_citation.entrydate,

T_citation.citvol,

Toxin Knowledge System Source Code

```
cpage1, cpage2,
T_citation.citdate,
T_citation.citnumb,
T_citation.citfile,
ctitle1, ctitle2, ctitle3, ctitle4
FROM
    citsource, citlocate, entrydate, citvol, citpage, cp2,
    citdate, citnumb, citfile, cittitle, ct2, ct3, ct4
ON Key(interrupt)
    let sw = 1
    exit input
ON Key(control-w)
    case
        when infield(citnumb)
            call showhelp(112)
        when infield(citsource)
            call showhelp(100)
        when infield(citlocate)
            call showhelp(101)
        when infield(citvol)
            call showhelp(102)
        when infield(citpage)
            call showhelp(103)
        when infield(cp2)
            call showhelp(103)
        when infield(citdate)
            call showhelp(104)
        when infield(cittitle)
            call showhelp(105)
    end case

before field citsource:
MESSAGE "Enter source code OR journal> F5/Cntl-F, book> F6/Cntl-B, Help> Ctrl-w."
ON Key(F5,CONTROL-F)
    if infield(citsource) then
        let T_citation.citsource= see_journ()
        OPTIONS help key CONTROL-W
        next field citsource
    end if
ON Key(F6,CONTROL-B)
    if infield(citsource) then
        let T_citation.citsource= see_book()
        next field citsource
    end if
after field citsource
message ""
case
    when T_citation.citsource[1,1] = "J"
        select jabrv into tmpname from journalst
        where journalst.jcode = T_citation.citsource
        if status=NOTFOUND then
            ERROR "Not currently in vocabulary"
        next field citsource
        end if
        display by name tmpname
    exit case
```

```

when T_citation.citsource[1,1] = "B"
    select bname into tmpname from booklst
    where booklst.bcode = T_citation.citsource
    if status=NOTFOUND then
        ERROR "Not currently in vocabulary"
    next field citsource
    end if
    display by name tmpname
    exit case
otherwise
    ERROR "Not a Journal or Book!!!"
    next field citsource
    exit case
END case
before field citvol
    let cvol = "0000"
after field citvoi
    let len1 = length(T_citation.citvol)-1
    let cvol[4-len1,4] = T_citation.citvol
    display by name T_citation.citvol
before field citpage
    let cpage3 = "00000"
after field citpage
    let len2 = length(cpage1)-1
    let x = cpage1
    let cpage3[5-len2,5] = cpage1
    display cpage1 to citpage
    let T_citation.citpage = cpage1 clipped, "-"
after field cp2
    let y = cpage2
    let len3 = length(cpage2)-1
    let T_citation.citpage = T_citation.citpage clipped, cpage2
    if y < x
        then error beep, "Last page less than first page!!!"
        next field citpage
    end if
    display cpage2 to cp2
after field citdate
    let thisyear = year(today) using "####"
    if T_citation.citdate < "1000" or T_citation.citdate > thisyear
        then
            ERROR beep, "Not a valid year!!!"
        next field citdate
    else
        let T_citation.citnumb = T_citation.citsource clipped, "-",
            cvol, "-",
            cpage3, "-",
            T_citation.citdate
        display by name T_citation.citnumb
    end if
after field citnumb
    if T_citation.citnumb is not null
        then
            let argcit = T_citation.citnumb clipped, "%"
            call exist_citnumb(argcit) returning cnt
            if cnt >= 1 then
                call citnumb_exists(argcit)
            end if
        end if
    end if

```

Toxin Knowledge System Source Code

```
        current window is cit1
        display "" at 1,1
    end if
    let tmp_add = " "
    if length(T_citation.citnumb) > 22
        then let tmp_add = ".",T_citation.citnumb[24]
    end if
    let T_citation.citfile = auth1[1,4] clipped,".",
        T_citation.citvol clipped,".",
        cpage1 clipped,".",
        T_citation.citdate[3, 4],
        tmp_add
    display by name T_citation.citfile
else
    error beep,"Must have citation number!"
    next field citdate
end if
after field citfile
    if T_citation.citfile is not null
        then
            let argfile = T_citation.citfile clipped, "%"
            call exist_citfile(argcit) returning cnt
            if cnt >= 1 then
                call citfile_exists(argfile)
                current window is cit1
                display "" at 1,1
            end if
        else
            error beep, "Must have citation file number!"
            next field citdate
        end if
    after input
        let T_citation.cittitle = ctitle1, ctitle2, ctitle3, ctitle4[1,61]
        let T_citation.citserial = 0
    END INPUT
options help key control-w
if sw = 1 then return end if
insert into citation values (T_citation.*)
let cc= status
    if cc < 0 then
        error cc
        return
    end if
MESSAGE "Row added"
SLEEP 1
MESSAGE ""
END FUNCTION
#####
FUNCTION flnd_cit(t_cit)
    define t_cit like citation.citnumb
    call cwinopen()
    case
        when t_cit is null
            OPTIONS input wrap,
            HELP file "tkshelp.msg"
            clear form
            let int_flag = 0
```

```

construct
  query1 on citnumb, citsource, citfile, citlocate,
    citvol, citpage, citdate, cittitle
  from citnumb, citsource, citfile, citlocate, citvol,
    citpage, citdate, cittitle
  prompt "For Journal codes <F5>, Bookcodes <F6>, else <Return> "
  for answer
    on key(F5,CONTROL-F)
      call see_journ()
    on key(F6,CONTROL-B)
      call see_book()
  end prompt
  if int_flag <> 0 then return end if
  let select1 = "select * from citation where ",
    query1 clipped
  let select2 = "select count(*) from citation where ",
    query1 clipped
  exit case
otherwise
  let select1 = "select * from citation where ",
    " citnumb = ", quote, t_cit, quote
  let select2 = "select count(*) from citation where ",
    " citnumb = ", quote, t_cit, quote
  exit case
end case
prepare cit_find from select1
prepare cit_cnt from select2
display " Searching... " at 15,2 attribute(reverse)
declare cit_curs cursor for cit_cnt
foreach cit_curs into cnt end foreach
declare c_curs SCROLL CURSOR FOR cit_find
open c_curs
CALL view_cit()
END FUNCTION
#####
FUNCTION view_cit()
  define
    arg like citation.citnumb,
    cc integer
  FETCH FIRST c_curs into T_citation.*
  if status = NOTFOUND
    THEN
      MESSAGE "No citation found."
      SLEEP 1
      MESSAGE ""
    ELSE
      CALL distitle()
      let tmp_cnt = 1
      display "" at 15,2
      display " ", cnt, " rows found." at 15, 2 attribute(reverse)
    end if
  MENU "BROWSE"
  COMMAND "Next"
    "View the next Citation in the list." HELP 170
  display " Searching ..." at 15,50 attribute(reverse)
  FETCH NEXT c_curs INTO T_citation.*
  let tmp_cnt = tmp_cnt + 1

```

Toxin Knowledge System Source Code

```
IF status = NOTFOUND THEN
    MESSAGE "No more Citations in this direction."
    SLEEP 1
    let tmp_cnt = cnt
    MESSAGE ""
    FETCH LAST c_curs INTO T_citation.*
    END IF
    call distitle()
    display "" at 15,2
    display " ",tmp_cnt, " of ", cnt, " rows" at 15,4
    attribute(reverse)
COMMAND "Previous"
    "View the Previous Citation in the list." HELP 170
    display " Searching ..." at 15,50 attribute(reverse)
    FETCH PREVIOUS c_curs INTO T_citation.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
        MESSAGE "No more Citations in this direction."
        SLEEP 1
        MESSAGE ""
        let tmp_cnt = 1
        FETCH FIRST c_curs INTO T_citation.*
        END IF
        call distitle()
        display " ",tmp_cnt, " of ", cnt, " rows" at 15,2
        attribute(reverse)
COMMAND "First"
    "View the first Citation in the list." HELP 170
    display " Searching ..." at 15,50 attribute(reverse)
    FETCH FIRST c_curs INTO T_citation.*
    let tmp_cnt = 1
    call distitle()
    display " ",tmp_cnt, " of ", cnt, " rows" at 15,2
    attribute(reverse)
COMMAND "Last"
    "View the Last Citation in the list." HELP 170
    display " Searching ..." at 15,50 attribute(reverse)
    • message "Searching for last record...."
    FETCH LAST c_curs INTO T_citation.*
    let tmp_cnt = cnt
    message ""
    call distitle()
    display " ",tmp_cnt, " of ", cnt, " rows" at 15,2
    attribute(reverse)
command "Update"
    "Update citation data" HELP 171
    call update_cit(T_citation.citserial)
command "Delete"
    "Delete this entry from database <submenu>" HELP 172
    menu "DELETE-JOURNAL-CIT"
        command "This-Table"
            "Delete just the data in the citation table" HELP 174
            call delete_cit(T_citation.citserial)
            exit menu
        command "All-Tables"
            "Delete all information in database related to this entry <DANGER>!" HELP 175
            call delete_all(T_citation.citnumb)
```

```

        exit menu
    command "Exit"
        "Exit Delete Submenu" HELP 2
    exit menu
end menu
COMMAND "Query-Again"
    "Enter new search criteria" HELP 176
    close c_curs
    let citnumber = ""
    call find_cit(citnumber)
    exit rmenu
COMMAND "Exit"
    "Leave this menu" HELP 2
    close c_curs
EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION update_cit(tmp_citserial)
    DEFINE
        ctitle1, ctitle2, ctitle3, ctitle4 char(63),
        cpage1, cpage2, tmp_page char(5),
        cvol char(4),
        citvol char(4),
        tmp_add char(2),
        jname like journalst.jabrv,
        bnme like booklst.bname,
        tmp_auth like authors.authname,
        argcit like citation.citnumb,
        argfile like citation.citfile,
        tmp_citnum like citation.citnumb,
        tmp_citfile like citation.citfile,
        c_cnt smallint,
        len1, len2, len3 smallint,
        cc, tmp_citserial integer
    #Initial setup
    MESSAGE ""
    let sw = 0
    let len1 = length(T_citation.citpage)
    for x = 1 to len1
        if T_citation.citpage[x] = "-" then
            let cpage1 = T_citation.citpage[1,x-1]
            if len1 > x
                then
                    let cpage2 = T_citation.citpage[x+1,len1]
                else
                    let cpage2 = "?"
                end if
            exit for
        end if
    end for
    let tmp_citfile = T_citation.citfile
    let tmp_citnum = T_citation.citnumb
    let ctitle1 = T_citation.cittitle[1,63]
    let ctitle2 = T_citation.cittitle[64,126]
    let ctitle3 = T_citation.cittitle[127,189]
    let ctitle4 = T_citation.cittitle[190,250]

```


Toxin Knowledge System Source Code

```
options input wrap,
  help file "tkshelp.msg",
  help key control-n
INPUT
  T_citation.citsource,
  T_citation.citlocate,
  T_citation.citvol,
  cpage1, cpage2,
  T_citation.citdate,
  T_citation.citnumb,
  T_citation.citfile
  ctitle1, ctitle2, ctitle3, ctitle4
WITHOUT DEFAULTS
FROM
  citsource, citlocate, citvol, citpage, cp2,
  citdate, citnumb, citfile, cittitle, ct2, ct3, ct4
on key(interrupt)
  let sw = 1
  exit input
ON Key(control-w)
  case
    when infield(citnumb)
      call showhelp(112)
    when infield(citsource)
      call showhelp(100)
    when infield(citlocate)
      call showhelp(101)
    when infield(citvol)
      call showhelp(102)
    when infield(citpage)
      call showhelp(103)
    when infield(cp2)
      call showhelp(103)
    when infield(citdate)
      call showhelp(104)
    when infield(cittitle)
      call showhelp(105)
  end case

before field citsource
  MESSAGE "Enter source code OR press F5 for journal, F6 for book help."
  ON Key(F5,CONTROL-F)
    if infield(citsource) then
      let T_citation.citsource = see_journ()
      next field citsource
    end if
  ON Key(F6,CONTROL-B)
    if infield(citsource) then
      call see_book() returning T_citation.citsource
      next field citsource
    end if
after field citsource
  if T_citation.citsource[1,1] = "J"
    then
      select jabrv into jnme from journalst
      where journalst.jcode = T_citation.citsource
      display jnme to tmpname
```

```

else
    select bname into bnme from booklst
    where booklst.bcode = T_citation.citsource
    display bnme to tmpname
end if
before field citvol
for x = 1 to 4
    if T_citation.citvol[x] <> "0" then
        let T_citation.citvol = T_citation.citvol[x,4]
        display by name T_citation.citvol
        exit for
    end if
end for
let cvol = "0000"
after field citvol
let len1 = length(T_citation.citvol)-1
let cvol[4-len1,4] = T_citation.citvol
display by name T_citation.citvol
before field citpage
if cpage1[1] = "0" then
    for x = 1 to 5
        if cpage1[x] <> "0" then
            let cpage1 = cpage1[x,5]
            let tmp_page = cpage1
            display tmp_page to citpage
            exit for
        end if
    end for
end if
after field citpage
let T_citation.citpage = cpage1
let len2 = length(T_citation.citpage)-1
let cpage1 = "00000"
let cpage1[5-len2,5] = T_citation.citpage
let tmp_page = T_citation.citpage
display T_citation.citpage to citpage
let T_citation.citpage = T_citation.citpage clipped, "-"
before field cp2
if cpage2[1] = "0" then
    for x = 1 to 5
        if cpage2[x] <> "0" then
            let cpage2 = cpage2[x,5]
            display cpage2 to cp2
            exit for
        end if
    end for
end if
after field cp2
if cpage2 < cpage1
    then
        error beep, "Last page less than first page!!!"
        next field citpage
    else
        display cpage2 to cp2
        let T_citation.citpage =
            T_citation.citpage clipped, cpage2 clipped
    end if

```

Toxin Knowledge System Source Code

```

after field citdate
  let T_citation.citnumb = T_citation.citsource clipped,"-",
    cvol,"-",
    cpagel,"-",
    T_citation.citdate
  display T_citation.citnumb to citnumb
after field citnumb
  if T_citation.citnumb is null
    then
      error beep, "Must have citation number!"
      next field citdate
    else
      if T_citation.citnumb <> tmp_citnum
        then
          let argcit = T_citation.citnumb clipped,"%%"
          select count(*) into cnt from citation
            where citnumb like argcit
          if cnt >= 1
            then
              call citnumb_exists(argcit)
              current window is cit1
              display "" at 1,1
            end if
          end if
          select authnam into tmp_auth
            from authors
            where aucitnumb = tmp_citnum
            and authsig = 1
          if status = NOTFOUND
            then let tmp_auth = "ANON"
          end if
          for x = 2 to 4
            if tmp_auth[x] = " "
              then
                let tmp_auth = tmp_auth[1,x-1]
              exit for
            end if
          end for
          if length(T_citation.citnumb) > 22
            then let tmp_add = ","T_citation.citnumb[24]
          end if
          let T_citation.citfile = tmp_auth[1,4] clipped,".",
            T_citation.citvol clipped,".",
            tmp_page clipped,".",
            T_citation.citdate[3, 4],
            tmp_add
          display by name T_citation.citfile
        end if
      after field citfile
        if T_citation.citfile is null
          then
            error beep, "Must have citation file number!"
            next field citdate
          else
            if T_citation.citfile <> tmp_citfile
              then
                let argfile = T_citation.citfile clipped,"%%"

```

```

        select count(*) into cnt from citation
        where citfile like argfile
        if cnt >= 1
        then
            call citfile_exists(argfile)
            current window is cit1
            display "" at 1,1
        end if
    end if
end if
after input
    let T_citation.cittitle = ctitle1,ctitle2,ctitle3,ctitle4[1,61]
END INPUT
options help key control-w
if sw = 1 then return end if
UPDATE citation set citation.* = T_citation.*
where citation.citserial = tmp_citserial
# update other tables
    UPDATE authors
        set aucitnumb = T_citation.citnumb,
        aucitfile = T_citation.citfile
        where aucitnumb = tmp_citnum
    UPDATE keywords
        set keycitnumb = T_citation.citnumb,
        keycitfile = T_citation.citfile
        where keycitnumb = tmp_citnum
    UPDATE paperover
        set papcitnumb = T_citation.citnumb,
        papcitfile = T_citation.citfile
        where papcitnumb = tmp_citnum
    UPDATE stdydsgn
        set stycitnumb = T_citation.citnumb,
        stycitfile = T_citation.citfile
        where stycitnumb = tmp_citnum
    UPDATE subjgrp
        set sgcitnumb = T_citation.citnumb
        where sgcitnumb = tmp_citnum
    UPDATE exporegm
        set excitnumb = T_citation.citnumb
        where excitnumb = tmp_citnum
    UPDATE expogrp
        set egcitnumb = T_citation.citnumb
        where egcitnumb = tmp_citnum
    UPDATE clinfind
        set cfcitnumb = T_citation.citnumb
        where cfcitnumb = tmp_citnum
    UPDATE tkacomment
        set cocitnumb = T_citation.citnumb,
        cocitfile = T_citation.citfile
        where cocitnumb = tmp_citnum
MESSAGE "Row updated"
SLEEP 1
MESSAGE ""
let citnumber = T_citation.citnumb
# Author data update option
    call auwinopen()
    call see_auth(citnumber)

```

Toxin Knowledge System Source Code

```
prompt "Do you want to update authors? (y/n) " for char answer
if upshift(answer) = "Y" then
    call update_auth(citnumber)
    call auwinclose()
end if
# Keyword data update option
let citnumber = T_citation.citnumb
call keywinopen()
call see_keys(citnumber)
prompt "Do you want to update keywords? (y/n) " for char answer
if upshift(answer) = "Y" then
    call update_key(citnumber)
    call keywinclose()
end if
end FUNCTION
#####
FUNCTION delete_cit(tmp_citserial)
    Define answer char(1),
        tmp_citserial integer

    PROMPT "Are you sure you want to delete this entry? (y/n) " for answer
    IF upshift(answer) = "N"
        then
            CLEAR FORM
            MESSAGE "Row NOT deleted."
            sleep 1
            MESSAGE ""
            RETURN
        else
            DELETE FROM citation where citserial = tmp_citserial
            clear form
            MESSAGE "Row deleted."
            SLEEP 1
            MESSAGE ""
        end if
    END FUNCTION
#####
FUNCTION distitle()
    define
        ctit1,ctit2,ctit3,ctit4 char(63),
        cpg1,cpg2 char(5),
        len1 smallint,
        authors,keywords,paperover,designs smallint,
        subjects,exposures,signs smallint,
        tmp_name char(60)
    current window is cit1
    let ctit1 = T_citation.cittitle[1,63]
    let ctit2 = T_citation.cittitle[64,126]
    let ctit3 = T_citation.cittitle[127,189]
    let ctit4 = T_citation.cittitle[190,250]
    let len1 = length(T_citation.citpage)
    if len1 > 0 then
        for x = 1 to len1
            if T_citation.citpage[x] = "-" then
                let cpg1 = T_citation.citpage[1,x-1]
                if len1 > x
                    then
```

```

        let cpg2 = T_citation.citpage[x+1,len1]
      else
        let cpg2 = "?"
      end if
    exit for
  end if
end for
end if
if T_citation.citsource[1,1] = "J"
  then
    select jabrv into tmp_name from journalst
      where jcode = T_citation.citsource
  else
    select bname into tmp_name from booklst
      where bcode = T_citation.citsource
  end if
display
  T_citation.citnumb,
  T_citation.citsource,
  T_citation.citfile,
  T_citation.citlocate,
  T_citation.entrydate,
  T_citation.citvol,
  cpg1, cpg2,
  T_citation.citdate,
  cit1, cit2, cit3, cit4,
  tmp_name
to
  citnumb, citsource, citfile, citlocate,
  entrydate, citvol, citpage, cp2,
  citdate, cititle, ct2, ct3, ct4, tmpname
#display "Counting..." at 15,50 attribute(reverse)
select count(*) into authors
  from authors
  where aucitnumb = T_citation.citnumb
display by name authors
select count(*) into keywords
  from keywords
  where keycitnumb = T_citation.citnumb
display by name keywords
select count(*) into paperover
  from paperover
  where papcitnumb = T_citation.citnumb
display by name paperover
select count(*) into designs
  from stdydsgn
  where stycitnumb = T_citation.citnumb
display by name designs
select count(*) into subjects
  from subjgrp
  where sgcitnumb = T_citation.citnumb
display by name subjects
select count(*) into exposures
  from exporegm
  where excitnumb = T_citation.citnumb
display by name exposures
select count(*) into signs

```

Toxin Knowledge System Source Code

```
from clinfind
where cfcitnumb = T_citation.citnumb
display by name signs
display "" at 15,50
END FUNCTION
```

#####

FUNCTION see_journ()

```
DEFINE j_list ARRAY[30] of RECORD
  jabrv like journalst.jabrv,
  jcode like journalst.jcode
end record,
holdjcode like journalst.jcode,
counter smallint
Open Window seej1 at 3,20 with form "jlist"
  attribute (border)
OPTIONS input wrap,
help file "tkshelp.msg"
MENU "J-LIST"
  command "Find" HELP 106
    let sw = 0
    clear form
    construct query1 on jabrv, jcode from j_listing[1].*
    let select1 = "select jabrv, jcode from journalst where ",
      query1 clipped
    prepare slct_4 from select1
    declare j_curs cursor for slct_4
    let counter = 1
    foreach j_curs into j_list[counter].*
      let counter = counter + 1
      if counter > 30 then
        exit foreach
      end if
    end foreach

    if counter = 1 then
      message "No Journal found with these first letters"
      sleep 2
      message "Try using "" to mean any sequence of characters"
      sleep 2
      continue menu
    end if
    call set_count(counter - 1)
    message "Highlight a journal abbreviation and press ESC"
    Display array j_list to j_listing.*
      on key(interrupt)
        let sw = 1
        exit display
    end display
    if sw = 1
      then next option "Find"
    else
      let counter = arr_curr()
      let holdjcode = j_list[counter].jcode
      message holdjcode
      exit menu
    end if
  command "Add" HELP 107
```

```

    let sw =0
    open window jw2 at 3,3 with form "vocjourn"
        attribute (Border)
    call add_journ()
    close window jw2
    let holdjcode = T_journalst.jcode
    message holdjcode
    exit menu
command "Select" HELP 108
    let sw =0
    call set_count(counter -1)
    message "Highlight a journal abbreviation and press ESC"
    Display array j_list to j_listing.*
        on key(interrupt)
            let sw = 1
            exit display
    end display
    if sw = 1
        then next option "Find"
    else
        let counter = arr_curr()
        let holdjcode = j_list[counter].jcode
        message holdjcode
        exit menu
    end if
command "Exit" HELP 2
    If sw = 0 then
        let holdjcode = NULL
    end if
    let sw =0
    exit menu
end menu
close window seej1
return holdjcode
END FUNCTION

```

```
#####
```

```

FUNCTION see_book()
    DEFINE b_list ARRAY[30] of RECORD
        bname like booklst.bname,
        bcode like booklst.bcode
    end record,
    holdbcode like booklst.bcode,
    counter smallint
    Open Window seeb1 at 3,20 with form "blist"
        attribute (border)
    MENU "B-LIST"
        command "Find" HELP 109
            let sw =0
            clear form
            construct query1 on bname, bcode from b_listing[1].*
            let select1 = "select bname, bcode from booklst where ",
                query1 clipped
            prepare slct_5 from select1
            declare b_curs cursor for slct_5
            let counter = 1
            foreach b_curs into b_list[counter].*
                let counter = counter + 1
            end foreach
        end menu
    end menu
END FUNCTION

```


Toxin Knowledge System Source Code

```
        if counter > 30 then
            exit foreach
        end if
    end foreach

    if counter = 1 then
        message "No Book found with these first letters"
        sleep 2
        continue menu
    end if
    call set_count(counter -1)
    message "Highlight a book abbreviation and press ESC"
    Display array b_list to b_listing.*
        on key(interrupt)
            let sw = 1
            exit display
        end display
    if sw = 1
        then next option "Find"
    else
        let counter = arr_curr()
        let holdbcode = b_list[counter].bcode
        message holdbcode
        exit menu
    end if
command "Add" HELP 110
let sw =0
open window bw2 at 3,3 with 20 rows, 68 columns
    attribute (Border)
    open form s_book from "bookadd"
    display form s_book
    call add_book()
    close window bw2
    let holdbcode = T_booklst.bcode
    message holdbcode
    exit menu
command "Select" HELP 111
let sw =0
call set_count(counter -1)
message "Highlight a book abbreviation and press ESC"
Display array b_list to b_listing.*
    on key(interrupt)
        let sw = 1
        exit display
    end display
if sw = 1
    then next option "Find"
else
    let counter = arr_curr()
    let holdbcode = b_list[counter].bcode
    message holdbcode
    exit menu
end if
command "Exit" HELP 2
if sw = 0 then
    let holdbcode = NULL
end if
```

```

        let sw =0
        exit menu
    end menu
close window seeb1
return holdbcode
END FUNCTION
#####
FUNCTION get_auth1()
    define auth1 like authors.authname
    call alrt260p1op()
    display "Please enter last name of first author." at 1,1
    prompt "> " for auth1
    let auth1 = upshift(auth1)
    call alrt260p1cl()
    return auth1
END FUNCTION
#####
FUNCTION citnumb_exists(c_num)
    define c_num like citation.citnumb
    error "Information for that citation number has already been entered!"
    sleep 1
    call show_fullcit2(c_num)
END FUNCTION
#####
FUNCTION citfile_exists(c_file)
    define c_file like citation.citfile
    error "Information for that file number has already been entered!"
    call show_file(c_file)
END FUNCTION
#####
FUNCTION exist_citnumb(c_cit)
    define c_cit like citation.citnumb,
        does_exist smallint
    select count(*) into does_exist
    from citation
    where citnumb like c_cit
    {
        if does_exist = 0
            then error beep,"No CITATION with that NUMBER"
            sleep 2
        end if
    }
    return does_exist
END FUNCTION
#####
FUNCTION exist_citfile(c_cit)
    define c_cit like citation.citfile,
        does_exist smallint
    select count(*) into does_exist
    from citation
    where citfile like c_cit
    {
        if does_exist = 0
            then error beep,"No CITATION with that NUMBER"
            sleep 2
        end if
    }

```

Toxin Knowledge System Source Code

```
return does_exist  
END FUNCTION
```

#tksauth.4gl

```
{  
TITLE: tksauth.4gl  
Copyright Harold L. Trammel, 1987-1988  
University of Illinois, CVM, IAPIC  
Funded by US Army Contract DAMD-17-C-7114  
Contains the following functions:
```

```
    add_auth(a_cit)  
    find_auth(a_cit)  
    view_auth()  
    disp_auth(a_cit)  
    update_auth(a_cit)  
    renum_auths()  
    delete_auth(a_cit)  
    see_auth(c_num)
```

```
}  
DATABASE tkstest  
GLOBALS "tksglob.4gl"
```

```
#-----#
```

FUNCTION add_auth(a_cit)

```
define
```

```
    a_cit like authors.aucitnumb,  
    R_authnumb like authors.aucitnumb,  
    R_authfile like authors.aucitfile,  
    tmp_cnt, cnt, numauth smallint
```

```
let sw = 0
```

```
call auwinopen()
```

```
clear form
```

```
display a_cit to aucitnumb
```

```
select citfile into citfileno from citation
```

```
    where citnumb = a_cit
```

```
display citfileno to aucitfile
```

```
if a_cit is null then
```

```
    options
```

```
        input no wrap
```

```
    clear form
```

```
    input R_authnumb, R_authfile from aucitnumb, aucitfile
```

```
        on key(interrupt)
```

```
            clear screen
```

```
            let sw = 1
```

```
            exit input
```

```
    end input
```

```
    options input wrap
```

```
    let a_cit = R_authnumb
```

```
    let citfileno = R_authfile
```

```
else
```

```
    let R_authnumb = a_cit
```

```
    let R_authfile = citfileno
```

```
end if
```

```
options input no wrap
```

```
for cnt = 1 to 10
```

```
    initialize a_array[cnt].* to null
```

```
end for
```

```

call set_count(10)
options
    help file "tkshe.p.msg"
{    help key F4 }

input array a_array from a_listing.* HELP 200
    on key(interrupt)
        clear screen
        let sw = 1
        return
display R_authnumb to aucitnumb
display R_authfile to aucitfile
before field authname
    let curr_arr = arr_curr()
after field authname
    let a_array[curr_arr].sig = arr_curr()
    let scr_arr = scr_line()
before field authsig
    display a_array[curr_arr].sig to a_listing[scr_arr].authsig
after delete
    call renum_auths()
after insert
    call renum_auths()
after input
    let numauth = arr_count()
end input
if sw = 1 then return
end if
for tmp_cnt = 1 to numauth
    if a_array[tmp_cnt].auth is not null
    then
        insert into authors values (R_authnumb, R_authfile,0,
                                   a_array[tmp_cnt].auth,
                                   a_array[tmp_cnt].sig)
    end if
end for
end FUNCTION
#-----#
FUNCTION find_auth(t_cit)
define t_cit like authors.authname
call auwinopen()
case
    when t_cit is null
        clear form
        let int_flag = 0
        construct query1 on aucitnumb, aucitfile, authname, authsig
            from aucitnumb, aucitfile, authname, authsig
            if int_flag <> 0 then return end if
        let select1 = "select * from authors where ",
            query1 clipped
        let select2 = "select count(*) from authors where ",
            query1 clipped
        exit case
    otherwise
        let select1 = "select * from authors where ",
            " aucitnumb = ",quote, t_cit clipped, quote
        let select2 = "select count(*) from authors where ",

```

Toxin Knowledge System Source Code

```
" aucitnumb = ", quote, t_cit clipped, quote
exit case
end case
prepare select_auth from select1
prepare au_cnt from select2
display "Searching . . . . . " at 11,2 attribute(reverse)
declare at_curs cursor for au_cnt
foreach at_curs into cnt
end foreach
declare auth_curs scroll cursor for select_auth
let chosen = false
open auth_curs
    call view_auth()
end FUNCTION
#-----#
FUNCTION view_auth()
define cc integer
fetch first auth_curs into T_authors.*
let cc=status
if (cc < 0) then error cc
end if
if status = notfound then
    message "No citation found."
    sleep 1
    message ""
else
    display " ", cnt, " rows found" at 11,2 attribute(reverse)
    display "ESC to continue" at 11,22 attribute(reverse)
    call disp_auth(T_authors.aucitnumb)
    let tmp_cnt = 1
    display "" at 11,2
end if
menu "BROWSE"
    command "Next" "View the next Author in the list." HELP 170
        fetch next auth_curs into T_authors.*
        let tmp_cnt = tmp_cnt + 1
        if status = notfound then
            message "No more Authors in this direction."
            sleep 1
            let tmp_cnt = cnt
            message ""
            fetch last auth_curs into T_authors.*
        end if
        display " ",tmp_cnt," of ",cnt," rows" at 11,2 attribute(reverse)
        call disp_auth(T_authors.aucitnumb)
        display "" at 11,3
    command "Previous" "View the Previous Author in the list." HELP 170
        fetch previous auth_curs into T_authors.*
        let tmp_cnt = tmp_cnt - 1
        if status = notfound then
            message "No more Authors in this direction."
            sleep 1
            message ""
            let tmp_cnt = 1
            fetch first auth_curs into T_authors.*
        end if
        display " ",tmp_cnt," of ",cnt," rows" at 11,2 attribute(reverse)
```

```

    call disp_auth(T_authors.aucitnumb)
    display "" at 11,2
command "First" "View the first Author in the list." HELP 170
    message "Searching for first record...." attribute(reverse)
    fetch first auth_curs into T_authors.*
    let tmp_cnt = 1
    message ""
    display " ",tmp_cnt," of ",cnt," rows" at 11,2 attribute(reverse)
    call disp_auth(T_authors.aucitnumb)
    display "" at 11,3
command "Last" "View the Last Author in the list." HELP 170
    message "Searching for last record...." attribute(reverse)
    fetch last auth_curs into T_authors.*
    let tmp_cnt = cnt
    message ""
    display " ",tmp_cnt," of ",cnt," rows" at 11,2 attribute(reverse)
    message ""
    call disp_auth(T_authors.aucitnumb)
    display "" at 11,3
command "Update" "Add, Modify, or Remove Authors in Existing Citation" HELP 171
    call update_auth(T_authors.aucitnumb)
command "Delete" "Delete ALL authors for a given citation" HELP 205
    call delete_auth(T_authors.aucitnumb)
command "Query-Again" "Enter new search criteria" HELP 176
    close auth_curs
    let citnumber = ""
    call find_auth(citnumber)
    exit menu
command "Exit" "Leave this menu" HELP 2
    close auth_curs
    exit menu
end menu
end FUNCTION
#-----#
FUNCTION disp_auth(a_cit)
define
    a_cit like authors.aucitnumb,
    counter smallint
clear form
let a_cit = T_authors.aucitnumb
let citfileno = T_authors.aucitfile
display a_cit to aucitnumb
display citfileno to aucitfile
declare au_curs cursor for
    select authname, authsig from authors
    where aucitnumb = a_cit
    order by authsig
let counter = 1
foreach au_curs into a_array[counter].*
    let counter = counter + 1
    if counter > 10 then
        exit foreach
    end if
end foreach
call set_count(counter - 1)
display "ESC to continue" at 11,22 attribute(reverse)
display array a_array to a_listing.*

```

Toxin Knowledge System Source Code

```
    on key(interrupt)
        exit display
end display
close au_curs
end FUNCTION
#-----#
FUNCTION update_auth(a_cit)
define
    a_cit, tmp_citnum like authors.aucitnumb,
    cite like authors.aucitfile,
    counter smallint
message ""
let sw = 0
let tmp_citnum = a_cit
options input no wrap
display a_cit to aucitnumb
select citfile into cite from citation
    where citation.citnumb = a_cit
display cite to aucitfile
input a_cit, cite without defaults from aucitnumb, aucitfile
    on key(interrupt)
        let sw = 1
        exit input
    after field aucitnumb
        if a_cit is null then
            next field aucitnumb
            message "MUST have number!!!"
        end if
        if a_cit <> tmp_citnum then
            call exist_citnumb(a_cit) returning x
            if x = 0
                then
                    error "No CITATION entered with this number"
                    next field aucitnumb
                else
                    select count(*) into x
                    from authors
                    where aucitnumb = a_cit
                    if x > 0
                        then
                            error "Author data already exists for this number."
                            next field aucitnumb
                        end if
                    end if
                end if
            end if
        end input
    if sw = 1 then return end if
message ""
options input wrap
input array a_array without defaults from a_listing.*
    on key(interrupt)
        let sw = 1
        exit input
    display "ESC to continue" at 11,22 attribute (reverse)
before field authname
    let curr_arr = arr_curr()
    let scr_arr = scr_line()
```

```

after field authname
    let a_array[curr_arr].sig = arr_curr()
    let scr_arr = scr_line()
before field authsig
    display a_array[curr_arr].sig to a_listing[scr_arr].authsig
after insert
    call renum_auths()
after delete
    call renum_auths()
end input
if sw = 1 then return end f
delete from authors
    where aucitnumb = tmp_citnum
for counter = 1 to arr_count()
    if a_array[counter].auth is not null
    then
        insert into authors
            values (a_cit,cite,0,
                a_array[counter].auth,
                a_array[counter].sig)
    end if
end for
end FUNCTION
#-----#
FUNCTION renum_auths()
define a_cur, a_cnt, s_lin, s_tot, ksmallint
let a_cur = arr_curr()
let a_cnt = arr_count()
let s_lin = scr_line()
let s_tot = 4
for k = a_cur to a_cnt
    let a_array[k].sig = k
    if s_lin <= s_tot then
        display k to a_listing[s_lin].authsig
        let s_lin = s_lin + 1
    end if
end for
end FUNCTION
#-----#
FUNCTION delete_auth(a_cit)
define answer char(1),
    a_cit like authors.aucitnumb
Prompt "Delete ALL author entries for this Citation (y/n) " for answer
if upshift(answer) = "Y" then
    delete from authors where aucitnumb = a_cit
    clear form
    message "ROW DELETED!"
    sleep 1
    Message ""
else
    clear form
    message "Row NOT deleted."
    sleep 1
    Message ""
    return
end if
end FUNCTION

```


Toxin Knowledge System Source Code

```
#-----#  
FUNCTION see_auth(c_num)  
  define c_num like authors.aucitnumb  
  call auwinopen()  
  clear form  
  display c_num to aucitnumb  
  display "Hit ESC to leave array." at 11,10 attribute(reverse)  
  declare au_see cursor for  
    select * from authors  
    where aucitnumb = c_num  
    order by authsig  
  let counter = 1  
  foreach au_see into  
    T_authors.aucitnumb,  
    T_authors.aucitfile,  
    T_authors.auserial,  
    a_array[counter].auth,  
    a_array[counter].sig  
    let counter = counter + 1  
    if counter > 10 then  
      exit foreach  
    end if  
  end foreach  
  display by name T_authors.aucitfile  
  call set_count(counter - 1)  
  display array a_array to a_listing.*  
    on key(interrupt)  
    exit display  
  end display  
  close au_see  
end FUNCTION
```

#tkskey.4gl

{TITLE: tkskey.4gl

Copyright Harold L. Trammel, 1987-1988

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Contains the following functions:

```

add_key(k_cit)
find_key(t_cit)
view_key()
disp_key(k_cit)
update_key(k_cit)
delete_key(k_cit)
seekeylist()
see_keys(c_num)

```

}

DATABASE tkstest

GLOBALS "tksglob.4gl"

#####

FUNCTION add_key(k_cit)

define

```

k_cit like keywords.keycitnumb,
R_keynumb like keywords.keycitnumb,
R_keyfile like keywords.keycitfile,
tmp_keyword like keywords.keyword,
tmp_code like keywords.keycode,
numkey smallint

```

#initial setup

```

let sw = 0
call keywinopen()
clear form

```

display k_cit to keycitnumb

if citfileno is null

then

```

select citfile into citfileno from citation
where citnumb = k_cit
display citfileno to keycitfile

```

end if

if k_cit is null *

then

```

options input no wrap
clear form
input R_keynumb, R_keyfile from keycitnumb, keycitfile
on key(interrupt)
clear screen
let sw=1
exit input
end input
let k_cit = R_keynumb
let citfileno = R_keyfile

```

else

```

let R_keynumb = k_cit
let R_keyfile = citfileno

```

end if

for tmp_cnt = 1 to 20

```

initialize k_array[tmp_cnt].* to null
end for

```

Toxin Knowledge System Source Code

```
display R_keynumb to keycitnumb
display R_keyfile to keycitfile
options input wrap, help file "tkshelp.msg"
input array k_array from k_listing.* HELP 300
  on key(interrupt)
    exit input
  before field keycode
    let curr_arr = arr_curr()
    let scr_arr = scr_line()
  after field keycode
    if k_array[curr_arr].code is not null
      then
        let tmp_code = k_array[curr_arr].code
        select kword into tmp_keyword from keylist
          where keylist.kcode = tmp_code
        if status=NOTFOUND
          then
            call seekeylist() returning k_array[curr_arr].code
            display k_array[curr_arr].code
              to k_listing[scr_arr].keycode
            select kword into tmp_keyword from keylist
              where keylist.kcode = k_array[curr_arr].code
            let k_array[curr_arr].keys = tmp_keyword
            display tmp_keyword to k_listing[scr_arr].keyword
            next field keyword
          else
            display tmp_code to k_listing[scr_arr].keycode
            display tmp_keyword to k_listing[scr_arr].keyword
            let k_array[curr_arr].keys = tmp_keyword
            let k_array[curr_arr].code = tmp_code
          end if
        else
          next field keyword
        end if
    after field keyword
      if k_array[curr_arr].keys is not null
        then
          let tmp_keyword = k_array[curr_arr].keys
          select kcode into tmp_code from keylist
            where keylist.kword = tmp_keyword
          if status=NOTFOUND
            then
              message beep, "This is not an acceptable keyword"
            else
              let k_array[curr_arr].code = tmp_code
              let k_array[curr_arr].keys = tmp_keyword
              display tmp_code to k_listing[scr_arr].keycode
              display tmp_keyword to k_listing[scr_arr].keyword
            end if
          end if
        before insert
          let numkey = arr_count()
        end input
      if sw = 1 then return end if
      for tmp_cnt = 1 to numkey
        insert into keywords values
```

```

        (R_keynumb,
         R_keyfile,
         0,
         k_array[tmp_cnt].keys,
         k_array[tmp_cnt].code)
    end for
clear screen
END FUNCTION
#####
FUNCTION find_key(t_cit)
    define t_cit like keywords.keycitnumb
    case
        when t_cit is null
            call keywinopen()
            clear form
            message "Enter search criteria and hit ESC to search."
            let int_flag = 0
            construct query1 on keycitnumb, keycitfile, keycode, keyword
                from keycitnumb, keycitfile, keycode, keyword
            if int_flag <> 0 then return end if
            let select1 = "select * from keywords where ", query1 clipped
            let select2 = "select count(*) from keywords where ",
                query1 clipped
            exit case
        otherwise
            let select1 = "select * from keywords where ",
                " keycitnumb = ", quote, t_cit, quote
            let select2 = "select count(*) from keywords where ",
                " keycitnumb = ", quote, t_cit, quote
            call keywinopen()
            exit case
        end case
    prepare find_key from select1
    prepare key_cnt from select2
    display " Searching... " at 18,2 attribute(reverse)
    declare ky_curs cursor for key_cnt
    foreach ky_curs into cnt
        end foreach
    declare key_curs scroll cursor of find_key
    open key_curs
    call view_key()
    close key_curs
END FUNCTION
#####
FUNCTION view_key()
    fetch first key_curs into T_keywords.*
    if status = notfound
        then
            message "No citation found."
            sleep 1
            return
        end if
    message ""
    display " ", cnt, " rows found." at 18, 2 attribute(reverse)
    call disp_key(T_keywords.keycitnumb)
    let tmp_cnt = 1
    menu "BROWSE"

```

Toxin Knowledge System Source Code

```
command "Next"
  "View the next Keyword in the list." HELP 170
  fetch next key_curs into T_keywords.*
  let tmp_cnt = tmp_cnt + 1
  if status = notfound then
    message "No more Keywords in this direction."
    sleep 1
    let tmp_cnt = cnt
    message ""
    fetch last key_curs into T_keywords.*
  end if
  display "" at 18,2
  display " ",tmp_cnt, " of ", cnt, " rows" at 18,2
  attribute(reverse)
  call disp_key(T_keywords.keycitnumb)
  display "" at 18,3
command "Previous"
  "View the Previous Keyword in the list." HELP 170
  fetch previous key_curs into T_keywords.*
  let tmp_cnt = tmp_cnt - 1
  if status = notfound then
    message "No more Keywords in this direction."
    sleep 1
    message ""
    let tmp_cnt = 1
    fetch first key_curs into T_keywords.*
  end if
  display "" at 18,2
  display " ", tmp_cnt, " of ", cnt, " rows" at 18,2
  attribute(reverse)
  call disp_key(T_keywords.keycitnumb)
  display "" at 18,3
command "First"
  "View the first Keyword in the list." HELP 170
  fetch first key_curs into T_keywords.*
  let tmp_cnt = 1
  display "" at 18,2
  display " ",tmp_cnt, " of ", cnt, " rows" at 18,2
  attribute(reverse)
  call disp_key(T_keywords.keycitnumb)
  display "" at 18,3
command "Last"
  "View the Last Keyword in the list." HELP 170
  message "Searching for last record...."
  fetch last key_curs into T_keywords.*
  let tmp_cnt = cnt
  message ""
  display "" at 18,2
  display " ",tmp_cnt, " of ", cnt, " rows" at 18,2
  attribute(reverse)
  message ""
  call disp_key(T_keywords.keycitnumb)
  display "" at 18,3
command "Update"
  "Add, Modify, or Delete Keywords for This Citation" HELP 171
  call update_key(T_keywords.keycitnumb)
command "Delete"
```

```

        "Delete ALL Keywords for a Given Citation" HELP 305
        call delete_key(T_keywords.keycitnumb)
    command "Query-Again"
        "Enter new search criteria" HELP 176
        close key_curs
        let citnumber = ""
        call find_key(citnumber)
        exit menu
    command "Exit"
        "Leave this menu" HELP 2
        close key_curs
        exit menu
    end menu
END FUNCTION
#####
FUNCTION disp_key(k_cit)
    define
        counter smallint,
        k_cit like keywords.keycitnumb
    clear form
    let k_cit = T_keywords.keycitnumb
    let citfileno = T_keywords.keycitfile
    display k_cit to keycitnumb
    display citfileno to keycitfile
    declare ke_curs cursor for
        select keycode, keyword from keywords
        where keycitnumb = k_cit
    let counter = 1
    foreach ke_curs into k_array[counter].*
        let counter = counter + 1
        if counter > 20 then
            exit foreach
        end if
    end foreach
    call set_count(counter - 1)
    display "ESC to continue" at 18,20 attribute(reverse)
    display array k_array to k_listing.*
    on key(interrupt)
        exit display
    end display
    close ke_curs
END FUNCTION
#####
FUNCTION update_key(k_cit)
    define
        tmp_citnum like keywords.keycitnumb,
        k_cit like keywords.keycitnumb,
        cite like keywords.keycitfile,
        counter smallint,
        tmp_code like keywords.keycode,
        tmp_keyword like keywords.keyword
    message ""
    let tmp_citnum = k_cit
    options input no wrap
    display k_cit to keycitnumb
    select citfile into cite from citation
        where citation.citnumb = k_cit

```

Toxin Knowledge System Source Code

```
display cite to keycitfile
input k_cit, cite without defaults from keycitnumb, keycitfile
on key(interrupt)
  exit input
after field keycitnumb
  if k_cit is null
    then next field keycitnumb
      message "MUST have number!!!"
    end if
  if k_cit <> tmp_citnum
    then
      call exist_citnumb(k_cit) returning x
      if x = 0
        then
          error "CITATION does not exist for this number."
          sleep 2
          next field keycitnumb
        else
          select count(*) into x
            from keywords
            where keycitnumb = k_cit
          if > 0
            then
              error "Keywords for this citation number already exists"
              sleep 2
              next field keycitnumb
            end if
          end if
        end if
      end if
    end if
  end input
message ""
options input wrap
input array k_array without defaults from k_listing.*
on key(interrupt)
  exit input
before field keycode
  let curr_arr = arr_curr()
  let scr_arr = scr_line()
after field keycode
  if k_array[curr_arr].code is not null
    then
      let tmp_code = k_array[curr_arr].code
      select kword into tmp_keyword from keylist
        where keylist.kcode = tmp_code
      if status=NOTFOUND
        then
          call seekkeylist() returning k_array[curr_arr].code
          display k_array[curr_arr].code
            to k_listing[scr_arr].keycode
          select kword into tmp_keyword from keylist
            where keylist.kcode = k_array[curr_arr].code
          let k_array[curr_arr].keys = tmp_keyword
          display tmp_keyword to k_listing[scr_arr].keyword
          next field keyword
        else
          display tmp_code to k_listing[scr_arr].keycode
          display tmp_keyword to k_listing[scr_arr].keyword
```

```

        let k_array[curr_arr].keys = tmp_keyword
        let k_array[curr_arr].code = tmp_code
    end if
else
    next field keyword
end if
after field keyword
if k_array[curr_arr].keys is not null
then
    let tmp_keyword = k_array[curr_arr].keys
    select kcode into tmp_code from keylist
        where keylist.kword = tmp_keyword
    if status=notfound
    then
        message beep, "This is not an acceptable keyword"
    else
        let k_array[curr_arr].code = tmp_code
        let k_array[curr_arr].keys = tmp_keyword
        display tmp_code to k_listing[scr_arr].keycode
        display tmp_keyword to k_listing[scr_arr].keyword
    end if
end if
end if
end input
delete from keywords
where keycitnumb = tmp_citnum
for counter = 1 to arr_count()
insert into keywords values (k_cit,
    cite, 0,
    k_array[counter].keys,
    k_array[counter].code)
end for
END FUNCTION
#####
FUNCTION delete_key(k_cit)
define answer char(1),
    k_cit like keywords.keycitnumb
prompt "Delete ALL keywords for this citation (y/n) " for answer
if upshift(answer) = "N"
then
    clear form
    message "Row NOT deleted."
    sleep 1
    Message ""
    return
else
    delete from keywords where keycitnumb = k_cit
    clear form
    message "ROW DELETED!"
    sleep 1
    Message ""
end if
END FUNCTION
#####
FUNCTION seekkeyword()
define
    key_list array(30) of record
    kcode like keylist.kcode,

```


Toxin Knowledge System Source Code

```
kword like keylist.kword
end record,
holdkcode like keylist.kcode,
cont smallint
open window seek1 at 3,40
with form "seekeys" attribute (border, reverse)
menu "KEY-LIST"
  command "Find" HELP 302
    clear form
    construct query1 on kcode, kword from k_list[1].*
    let select1 = "select kcode, kword from keylist where ",
      query1 clippx 1
    prepare select_klist from select1
    declare k_curs cursor for select_klist
    let cont = 1
    foreach k_curs into key_list[cont].*
      let cont = cont + 1
      if cont > 30
        then
          exit foreach
        end if
      end foreach
    if cont = 1
      then
        message "No Keyword found with these first letters"
        sleep 2
        exit menu
      end if
    call set_count(cont-1)
    message "Highlight a keyword abbrev and hit ESC"
    display array key_list to k_list.*
    on key(interrupt)
      exit display
    end display
    let cont = arr_curr()
    let holdkcode = key_list[cont].kcode
    exit menu
  command "Add" HELP 303
    open window kw2 at 3,3 with 20 rows, 66 columns
      attribute (Border)
    open form s_key from "vockeys"
    display form s_key
    call add_klist()
    close window kw2
  command "Exit" HELP 2
    exit menu
  end menu
close window seek1
return holdkcode
END FUNCTION
#####
FUNCTION see_keys(c_num)
  define
    c_num like keywords.keycitnumb,
    c_fil like keywords.keycitfile,
    citfile like citation.citfile
  call keywinopen()
```

```
clear form
display c_num to keycitnumb
select unique(keycitfile) into citfile
  from keywords
  where keycitnumb = c_num
display citfile to keycitfile
display "ESC to continue" at 18,20 attribute(reverse)
declare key_see cursor for
  select keycode, keyword from keywords
  where keycitnumb = c_num
let counter = 1
foreach key_see into k_array[counter].*
  let counter = counter + 1
  if counter > 20 then exit foreach end if
end foreach
call set_count(counter -1)
display array k_array to k_listing.*
  on key(interrupt)
    exit display
  end display
close key_see
END FUNCTION
```

Toxin Knowledge System Source Code

#tksqlquery.4gl

```
{
TITLE: tksquery.4gl
Copyright Harold L. Trammel, 1987-1988
University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
Purpose: to provide a Query-by-example mechanism for citation.
authors, keywords
Contains the following functions:
    querybib()
    view_all()
    see_cit(c_num)
    out_cit(c_num,pf)
    top_down()
}
```

database tkstest

globals "tksglob.4gl"

#####

FUNCTION querybib()

```
    call qwinopen()
    let int_flag = 0
    construct query1 on
        #items
            citnumb, citfile, citsource, citvol, citpage, citdate, citlocate,
            cittitle, authname,
            keyword, keycode
    from
        citnumb, citfile, citsource, citvol, citpage, citdate, citlocate,
        ct1, authname,
        keyword, keycode
    let select1 = "select unique(citnumb), citfile, citserial, citvol, citpage, citdate, cittitle, citlocate",
        " from citation, authors, keywords where ",
        query1 clipped,
        " and citnumb = aucitnumb and citnumb = keycitnumb ",
        " order by citfile, citnumb"
    prepare select_all from select1
    if int_flag <> 0
        then return
    end if
    display " Searching ..." at 21,2 attribute(reverse)
    let cnt = 0
    declare q_cnt cursor for select_all
    foreach q_cnt into T_citation.*
        let cnt = cnt + 1
        if status = notfound
            then
                let cnt = 0
                exit foreach
            end if
        end foreach
    if int_flag <> 0
        then return
    end if
    declare q_curs scroll cursor for select_all
    open q_curs
    fetch first q_curs into T_citation.*
    if status = NOTFOUND
```

```

then
    message "No citation found."
    sleep 1
    message ""
else
    display " ", cnt, " citations found." at 21,2
    attribute(reverse)
    let tmp_cnt = 1
    call view_all()
end if
close q_curs
end FUNCTION
#####
FUNCTION view_all()
    call see_cit(T_citation.citnumb)
    let tmp_cnt = 1
    display "" at 21,2
    display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
    attribute(reverse)
    MENU "BROWSE"
    COMMAND "Next"
        "View the next Citation in the list." HELP 170
        display " Searching ..." at 21,2 attribute(reverse)
        FETCH NEXT q_curs INTO T_citation.*
        IF status = NOTFOUND THEN
            MESSAGE beep, "No more Citations in this direction."
            SLEEP 1
            MESSAGE ""
            FETCH LAST q_curs INTO T_citation.*
            END IF
        call see_cit(T_citation.citnumb)
        let tmp_cnt = tmp_cnt + 1
        display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
        attribute(reverse)
        message ""
    COMMAND "Previous"
        "View the Previous Citation in the list." HELP 170
        display " Searching ..." at 21,2 attribute(reverse)
        FETCH PREVIOUS q_curs INTO T_citation.*
        IF status = NOTFOUND THEN
            MESSAGE beep, "No more Citations in this direction."
            SLEEP 1
            MESSAGE ""
            FETCH FIRST q_curs INTO T_citation.*
            END IF
        call see_cit(T_citation.citnumb)
        let tmp_cnt = tmp_cnt - 1
        display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
        attribute(reverse)
        message ""
    COMMAND "First"
        "View the first Citation in the list." HELP 170
        display " Searching ..." at 21,2 attribute(reverse)
        FETCH FIRST q_curs INTO T_citation.*
        call see_cit(T_citation.citnumb)
        let tmp_cnt = 1
        display " ", tmp_cnt, " of ", cnt, " rows" at 21,2

```

Toxin Knowledge System Source Code

```
        attribute(reverse)
    message ""
    COMMAND "Last"
        "View the Last Citation in the list." HELP 170
        display " Searching ..." at 21,2 attribute(reverse)
        FETCH LAST q_curs INTO T_citation.*
        call see_cit(T_citation.citnumb)
        let tmp_cnt = cnt
        display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
        attribute(reverse)
    message ""
    COMMAND "Output"
        "Output selected data" HELP 1300
        call out_all(T_citation.citnumb)
    COMMAND "Exit"
        "Leave this menu" HELP 2
    EXIT MENU
END MENU
end FUNCTION
#####
FUNCTION see_cit(c_num)
    define
        cit1 char(50),
        cit2,cit3,cit4 char(70),
        tmpname char(70),
        c_num like citation.citnumb,
        auth_string, key_string char(500),
        atemp1, atemp2, atemp3 char(70),
        temp1, temp2, temp3 char(70)
    select * into T_citation.*
    from citation
    where citnumb = c_num
    let cit1 = T_citation.cititle[1,40]
    let cit2 = T_citation.cititle[41,110]
    let cit3 = T_citation.cititle[111,180]
    let cit4 = T_citation.cititle[181,250]
    if T_citation.citsource[1,1] = "J"
    then
        select jabrv into tmpname from journalst
        where jcode = T_citation.citsource
    else
        select bname into tmpname from booklst
        where bcode = T_citation.citsource
    end if
    declare au_see cursor for
    select * from authors
    where aucitnumb = c_num
    order by authsig
    let counter = 1
    let auth_string = ""
    foreach au_see into T_authors.*
        if counter = 1
        then
            let auth_string = T_authors.authname clipped
        else
            if (length(auth_string) + length(T_authors.authname)) > 497
            then exit foreach
        end if
        let auth_string = auth_string + T_authors.authname + " "
        let counter = counter + 1
    end foreach
    let key_string = " "
    let atemp1 = " "
    let atemp2 = " "
    let atemp3 = " "
```

```

        end if
        let auth_string = auth_string clipped, ", ",
            T_authors.authname clipped
    end if
    let counter = counter + 1
    if counter > 10 then exit foreach end if
end foreach
if length(auth_string) > 210
    then let auth_string[208,210] = "..."
end if
let atemp1 = auth_string[1,70]
let atemp2 = auth_string[71,140]
let atemp3 = auth_string[141,210]
close au_see
declare key_see cursor for
    select * from keywords
    where keycitnumb = c_num
let counter = 1
let key_string = ""
foreach key_see into T_keywords.*
    if counter = 1
        then
            let key_string = T_keywords.keyword clipped
        else
            if (length(key_string) + length(T_keywords.keyword)) > 497
                then exit foreach
            end if
            let key_string = key_string clipped, ", ",
                T_keywords.keyword clipped
        end if
        let counter = counter + 1
    if counter > 20 then exit foreach end if
end foreach
if length(key_string) > 210
    then let key_string[208,210] = "..."
end if
let temp1 = key_string[1,70]
let temp2 = key_string[71,140]
let temp3 = key_string[141,210]
close key_see
display
    #items
        T_citation.citnumb,
        T_citation.citsource,
        T_citation.citfile,
        T_citation.citlocat,
        T_citation.citvol,
        T_citation.citpage,
        T_citation.citdate,
        cit1, cit2, cit3, cit4,
        tmpname,
        atemp1, atemp2,
        temp1, temp2
to
    citnumb, citsource, citfile, citlocat, citvol, citpage,
    citdate, ct1, ct2, ct3, ct4, citname,
    authname, authname2,

```

Toxin Knowledge System Source Code

```
keyword, keyword2
end FUNCTION
#####
FUNCTION out_all(c_num)
define
    c_num like citation.citnumb,
    print_cnt smallint,
    fp char(30)
menu "OUTPUT"
    command "Printer"
        "Send data to line printer" HELP 1301
        menu "OUT-TO-PRINTER"
            command "This-Citation"
                "Send the displayed citation to printer" HELP 1302
                let fp = "cat > tmp.out"
                message "Printing .."
                call out_cit(c_num,fp)
                run "print tmp.out; rm tmp.out"
                exit menu
            command "All-Citations"
                "Send all citations from current query printer" HELP 1303
                let fp = "cat >> tmp.out"
                let print_cnt = 0
                declare outp_curs cursor for select_all
                foreach outp_curs into c_num
                    let print_cnt = print_cnt + 1
                    message "Printing ...", print_cnt
                    call out_cit(c_num,fp)
                end foreach
                run "print tmp.out; rm tmp.out"
                exit menu
            command "Exit" HELP 2
            exit menu
        end menu
    exit menu
command "File"
    "Send data to file" HELP 1304
    menu "OUT-TO-FILE"
        command "This-Citation"
            "Send the displayed citation to a file" HELP 1305
            MENU "FILE-SELECTION"
                command "New-File" HELP 1306
                    prompt "Send to what file > " for fp
                    message "Writing to file ", fp
                    let fp = "cat >", fp clipped
                    call out_cit(c_num,fp)
                    exit menu
                command "Append-to-File" HELP 1307
                    prompt "Send to what file > " for fp
                    message "Writing to file ", fp
                    let fp = "cat >>", fp clipped
                    call out_cit(c_num,fp)
                    exit menu
            command "Exit" HELP 2
            exit menu
        end menu
    command "All-Citations"
```

```

"Send all citations from current query to file" HELP 1308
MENU "FILE-SELECTION"
  command "New-File" HELP 1309
    prompt "Send to what file > " for fp
    let fp = "cat >>", fp clipped
    let print_cnt = 0
    declare outf_curs cursor for select_all
    foreach outf_curs into c_num
      let print_cnt = print_cnt + 1
      message "Writing ", print_cnt, " to file ", fp
      call out_cit(c_num,fp)
    end foreach
  exit menu
  command "Append-to-File" HELP 1310
    prompt "Send to what file > " for fp
    let fp = "cat >>", fp clipped
    let print_cnt = 0
    declare outaf_curs cursor for select_all
    foreach outaf_curs into c_num
      let print_cnt = print_cnt + 1
      message "Writing ", print_cnt, " to file ", fp
      call out_cit(c_num,fp)
    end foreach
  exit menu
  command "Exit" HELP 2
  exit menu
end menu
command "Exit" HELP 2
exit menu
end menu
exit menu
command "Exit" "Exit this window" HELP 2
exit menu
end menu
end FUNCTION
#####
FUNCTION out_cit(c_num,pf)
  define
    c_num like citation.citnumb,
    O_citation record like citation.*,
    pf char(30)
  declare out_curs cursor for
    select * from citation
    where citnumb = c_num
    order by citnumb
  start report cit_out to pipe pf
    foreach out_curs into O_citation.*
      output to report cit_out (O_citation.*)
    end foreach
  finish report cit_out
end FUNCTION

#####
REPORT cit_out(c_citation)
  define
    c_citation record like citation.*

```


Toxin Knowledge System Source Code

```
c_authors record like authors.*;
c_keywords record like keywords.*;
tmpname char(60),
a_string char(550),
k_string char(550),
hold_string char(1100),
tot_len, x, y smallint
output
report to "tks_query.out"
left margin 0
top margin 0
bottom margin 0
page length 10
order external by c_citation.citnumb
format
before group of c_citation.citnumb
let hold_string = ""
declare a_see cursor for
select * from authors
where aucitnumb = c_citation.citnumb
order by authsig
let counter = 1
let a_string = ""
foreach a_see into c_authors.*
if counter = 1
then
let a_string = c_authors.authname clipped
else
if (length(a_string) + length(c_authors.authname)) > 538
then
let a_string[538,540] = "..."
exit foreach
else
let a_string = a_string clipped, ", ",
c_authors.authname clipped
end if
end if
let counter = counter + 1
if counter > 10 then exit foreach end if
end foreach
close a_see
declare k_see cursor for
select * from keywords
where keycitnumb = c_citation.citnumb
let counter = 1
let k_string = ""
foreach k_see into c_keywords.*
if counter = 1
then
let k_string = c_keywords.keyword clipped
else
if (length(k_string) + length(c_keywords.keyword)) > 538
then
let k_string[538,540] = "..."
exit foreach
else
let k_string = k_string clipped, ", ",
```

```

        c_keywords.keyword clipped
    end if
    end if
    let counter = counter + 1
    if counter > 20 then exit foreach end if
end foreach
close k_see
after group of c_citation.citnumb
if c_citation.citsource[1,1] = "]"
then
    select jabrv into tmpname from journalst
    where jcode = c_citation.citsource
else
    select bname into tmpname from booklst
    where bcode = c_citation.citsource
end if
print
print "TKS code: ", c_citation.citnumb
print "File code: ", c_citation.citfile clipped, " in ",
    c_citation.citiocate clipped, " files "
print
let hold_string = a_string clipped, ":",
    c_citation.cittitle clipped, ":",
    tmpname: clipped, ":",
    c_citation.citvol, ":",
    c_citation.citpage, ":",
    c_citation.citdate
let tot_len = length(hold_string)
if tot_len >= 80
    then let y = 80
    else let y = tot_len
    end if
for x = 1 to tot_len step 80
    print hold_string[x,y]
    if tot_len - x < 80
        then let y = tot_len
        else let y = y + 80
        end if
    end for
let k_string = "Keywords: ", k_string clipped
let tot_len = length(k_string)
if tot_len >= 80
    then let y = 80
    else let y = tot_len
    end if
for x = 1 to tot_len step 80
    print k_string[x,y]
    if tot_len - x < 80
        then let y = tot_len
        else let y = y + 80
        end if
    end for
end report
*****
FUNCTION top_down()
( This section needs to have additional options )
let citnumber = ""

```

Toxin Knowledge System Source Code

```
call find_cit(citnumber)
menu "TOP_DOWN"
  command "Citation"
    "Find Citation to serve as top"
    let citnumber = ""
    call find_cit(citnumber)
  command "Authors"
    "See Authors for selected top"
    call find_auth(T_citation.citnumb)
  command "Keywords"
    "See Keywords for selected top"
    call find_key(T_citation.citnumb)
  command "PaperOver"
    "See Paper Overview for selected top"
    call find_paper(T_citation.citnumb)
  command "Design"
    "See Study Designs for selected top"
    call find_dsgn(T_citation.citnumb)
  command "Subjects"
    "See Subject Groups for selected top"
    call find_sgrp(T_citation.citnumb,0)
  command "Regimens"
    "See Exposure Regimens for selected top"
    call find_expo(T_citation.citnumb,0)
  command "Links"
    "See Exposure Groups for selected top"
    call find_exgp(T_citation.citnumb)
  command "Findings"
    "See Clinical Findings for selected top"
    call find_cfind(T_citation.citnumb)
  command "MoreData"
    "Add more data to the selected citation tables"
    call add_abs(T_citation.citnumb)
  command "Exit"
    "Exit this menu"
    exit menu
end menu
end function
```

#tkssshows.4gl

```
(
TITLE: tkssshows.4gl
Copyright Harold L. Trammel, 1987-1988
University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
```

Contains the following functions:

```
show_dsgn(p_cit, cur_pge)
gen_dsgdsc(p_cit, tmp_dsgn)
show_subj(s_cit, tmp_dsgn, cur_pge)
gen_subdsc(s_cit, tmp_dsgn, tmp_pge)
show_expo(e_cit, tmp_dsgn, cur_pge)
gen_expdsc(e_cit, tmp_dsgn, tmp_pge)
show_fullcit(t_cit)
show_fullcit2(in_cit)
show_file(in_file)
disp_fullcit(t_cit)
```

```
database tkstest
```

```
globals "tksglob.4gl"
```

```
#####
```

```
FUNCTION show_dsgn(p_cit, cur_pge)
```

```
define hold_dsgn char(650),
theCnt, x, y smallint,
tmp1,tmp2,tmp3,tmp4,tmp5,tmp6,tmp7,tmp8,tmp9,tmp10 char(65),
p_cit like paperover.papcitnumb,
tot_pge, cur_pge, cur_row, p_numdsgn, cc integer
select count(*) into p_numdsgn
from stdydsgn
where stycitnumb = p_cit
let tot_pge = p_numdsgn/10
case
when (cur_pge > tot_pge)
error "No more rows in this direction"
return tot_pge
exit case
when (cur_pge < 0)
error "No more rows in this direction"
return 0
exit case
end case
```

```
declare dsgn scroll cursor for
select * from stdydsgn
where stycitnumb = p_cit
order by stydsgncur
```

```
let x = 1
let theCnt = 0
let hold_dsgn = ""
open dsgn
for cur_row = (cur_pge*10+1) to (cur_pge*10+10)
if cur_row > p_numdsgn
then exit for
end if
fetch absolute cur_row dsgn into T_stdydsgn.*
let theCnt = theCnt + 1
```

Toxin Knowledge System Source Code

```
let hold_dsgn[x,x+4] = T_stdydsgn.stydsgncur using "<&"," = "
let hold_dsgn= hold_dsgn clipped,
    T_stdydsgn.stynumgrp using "<&"," GRP, ",
    T_stdydsgn.stynumexp using "<&"," EXP, ",
    T_stdydsgn.stycntl, " CNTL "
let x = theCnt * 65 + 1
end for
# Create values
let tmp1 = hold_dsgn[1,65]
let tmp2 = hold_dsgn[66,130]
let tmp3 = hold_dsgn[131,195]
let tmp4 = hold_dsgn[196,260]
let tmp5 = hold_dsgn[261,325]
let tmp6 = hold_dsgn[326,390]
let tmp7 = hold_dsgn[391,455]
let tmp8 = hold_dsgn[456,520]
let tmp9 = hold_dsgn[521,585]
let tmp10 = hold_dsgn[586,650]
# Display values
display tmp1 at 11,1 attribute(reverse)
display tmp2 at 12,1 attribute(reverse)
display tmp3 at 13,1 attribute(reverse)
display tmp4 at 14,1 attribute(reverse)
display tmp5 at 15,1 attribute(reverse)
display tmp6 at 16,1 attribute(reverse)
display tmp7 at 17,1 attribute(reverse)
display tmp8 at 18,1 attribute(reverse)
display tmp9 at 19,1 attribute(reverse)
display tmp10 at 20,1 attribute(reverse)
close dsgn
return cur_pge
END FUNCTION
#####
FUNCTION gen_dsgdac(p_cit, tmp_dsgn)
define
    hold_dsgn char(65),
    p_cit like paperover.papcitnumb,
    hold_styserial integer,
    tmp_dsgn smallint
declare gen_dsgn cursor for
select * from stdydsgn
where stycitnumb = p_cit
and stydsgncur = tmp_dsgn
foreach gen_dsgn into T_stdydsgn.*
let hold_dsgn= T_stdydsgn.stynumgrp using "<&"," GRP, ",
    T_stdydsgn.stynumexp using "<&"," EXP, ",
    T_stdydsgn.stycntl clipped, " CNTL "
let hold_styserial = T_stdydsgn.styserial
end foreach
return hold_dsgn, hold_styserial
END FUNCTION
#####
FUNCTION show_subj(a_cit, tmp_dsgn, cur_pge)
define
    hold_subj char(650),
    tmp_dsgn integer,
    theCnt, x, y smallint,
```

```

tmp1,tmp2,tmp3,tmp4,tmp5,tmp6,tmp7,tmp8,tmp9,tmp10 char(65),
s_cit like subjgrp.sgcitnumb,
tot_pge, cur_pge, cur_row, p_subnum, cc integer
select count(*) into p_subnum from subjgrp
where sgcitnumb = s_cit
and sgdsgnnum = tmp_dsgn
let tot_pge = p_subnum/10
case
  when (cur_pge > tot_pge)
    error "No more rows in this direction"
    return tot_pge
  exit case
  when (cur_pge < 0)
    error "No more rows in this direction"
    return 0
  exit case
end case
declare subj_curs scroll cursor for
select * from subjgrp
where sgcitnumb = s_cit
and sgdsgnnum = tmp_dsgn
order by sglink
let x = 1
let theCnt = 0
let hold_subj = ""
open subj_curs
for cur_row = (cur_pge*10+1) to (cur_pge*10+10)
  if cur_row > p_subnum
    then exit for
  end if
  fetch absolute cur_row subj_curs into T_subjgrp.*
  let theCnt = theCnt + 1
  let hold_subj(x,x+4) = T_subjgrp.sglink using "<&", " = "
  let hold_subj = hold_subj clipped,
    T_subjgrp.sgnumb using "<<<&", " ",
    T_subjgrp.sgspecies clipped, " ",
    "Age: ", T_subjgrp.sgage clipped, " ",
    T_subjgrp.sgageunit clipped, " ",
    "Wt: ", T_subjgrp.sgmt using "<<<<&.<<", " ",
    T_subjgrp.sgmtunit clipped, " ",
    "Sex: ", T_subjgrp.sgsex clipped, " ",
    T_subjgrp.sgtotexpo using "<&", " EXP"
  let x = theCnt * 65 + 1
end for
#Create values
let tmp1 = hold_subj(1,65)
let tmp2 = hold_subj(66,130)
let tmp3 = hold_subj(131,195)
let tmp4 = hold_subj(196,260)
let tmp5 = hold_subj(261,325)
let tmp6 = hold_subj(326,390)
let tmp7 = hold_subj(391,455)
let tmp8 = hold_subj(456,520)
let tmp9 = hold_subj(521,585)
let tmp10 = hold_subj(586,650)
#display values
display tmp1 at 11,1 attribute(reverse)

```

Toxin Knowledge System Source Code

```
display tmp2 at 12,1 attribute(reverse)
display tmp3 at 13,1 attribute(reverse)
display tmp4 at 14,1 attribute(reverse)
display tmp5 at 15,1 attribute(reverse)
display tmp6 at 16,1 attribute(reverse)
display tmp7 at 17,1 attribute(reverse)
display tmp8 at 18,1 attribute(reverse)
display tmp9 at 19,1 attribute(reverse)
display tmp10 at 20,1 attribute(reverse)
close subj_curs
return cur_pge
END FUNCTION
#####
FUNCTION gen_subdsc (s_cit, tmp_dsgn, tmp_subj)
define
    tmp_dsgn integer,
    hold_sgserial integer,
    hold_subj char(65),
    s_cit like subjgrp.sgcitnumb,
    tmp_subj smallint
declare gen_curs cursor for
select * from subjgrp
where sgcitnumb = s_cit
and sgdsgrnum = tmp_dsgn
and sglink = tmp_subj
foreach gen_curs into T_subjgrp.*
let hold_subj= T_subjgrp.sgrnumb using "<<<&", " ",
    T_subjgrp.sgspecies clipped, " ",
    "Age: ", T_subjgrp.sgage clipped, " ",
    T_subjgrp.sgageunit clipped, " ",
    "Wt: ", T_subjgrp.sgrwt using "<<<&.<<", " ",
    T_subjgrp.sgrwtunit clipped, " ",
    "Sex: ", T_subjgrp.sgsex clipped, " ",
    T_subjgrp.sgtotexpo using "<&", " EXP"
let hold_sgserial = T_subjgrp.sgserial
end foreach
return hold_subj, hold_sgserial
END FUNCTION
#####
FUNCTION show_expo(e_cit, tmp_dsgn, cur_pge)
define
    hold_expo char(650),
    tmp_dsgn integer,
    theCnt, x, y smallint,
    tmp1,tmp2,tmp3,tmp4,tmp5,tmp6,tmp7,tmp8,tmp9,tmp10 char(65),
    e_cit like exporegm.excitnumb,
    tot_pge, cur_pge, cur_row, p_expnum, cc integer
select count(*) into p_expnum from exporegm
where excitnumb = e_cit
and exdsgrnum = tmp_dsgn
let tot_pge = p_expnum/10
case
when (cur_pge > tot_pge)
error "No more rows in this direction"
return tot_pge
exit case
when (cur_pge < 0)
```

```

        error "No more rows in this direction"
        return 0
    exit case
end case
declare expo_curs scroll cursor for
select * from exporegm
where excitnumb = e_cit
and exdsgnnum = tmp_dsgn
order by exlink
let x = 1
let theCnt = 0
let hold_expo = ""
open expo_curs
for cur_row = (cur_pge*10+1) to (cur_pge*10+10)
    if cur_row > p_expnum
        then exit for
    end if
    fetch absolute cur_row expo_curs into T_exporegm.*
    let theCnt = theCnt + 1
    let hold_expo[x,x+4] = T_exporegm.exlink using "<&", " = "
    let hold_expo = hold_expo clipped,
        T_exporegm.exagent[1,20] clipped, ", ",
        T_exporegm.exdose clipped, " ",
        T_exporegm.exdoseunit clipped, " ",
        T_exporegm.exroute, ", given ",
        T_exporegm.exinterval clipped, " x ",
        T_exporegm.exduration[1,8] clipped
    let x = theCnt * 65 + 1
end for
#create values
let tmp1 = hold_expo[1,65]
let tmp2 = hold_expo[66,130]
let tmp3 = hold_expo[131,195]
let tmp4 = hold_expo[196,260]
let tmp5 = hold_expo[261,325]
let tmp6 = hold_expo[326,390]
let tmp7 = hold_expo[391,455]
let tmp8 = hold_expo[456,520]
let tmp9 = hold_expo[521,585]
let tmp10 = hold_expo[586,650]
#display values
display tmp1 at 11,1 attribute(reverse)
display tmp2 at 12,1 attribute(reverse)
display tmp3 at 13,1 attribute(reverse)
display tmp4 at 14,1 attribute(reverse)
display tmp5 at 15,1 attribute(reverse)
display tmp6 at 16,1 attribute(reverse)
display tmp7 at 17,1 attribute(reverse)
display tmp8 at 18,1 attribute(reverse)
display tmp9 at 19,1 attribute(reverse)
display tmp10 at 20,1 attribute(reverse)
close expo_curs
return cur_pge
END FUNCTION
#####
FUNCTION gen_expdsc(e_cit, tmp_dsgn, tmp_expo)
define

```


Toxin Knowledge System Source Code

```
hold_expo char(65),
tmp_dsgn integer,
hold_exserial integer,
e_cit like exporegm.excitnumb,
tmp_expo smallint
declare exp_curs cursor for
select * from exporegm
where excitnumb = e_cit
and exdsgnum = tmp_dsgn
and exlink = tmp_expo
foreach exp_curs into T_exporegm.*
let hold_expo= T_exporegm.exagent[1,20] clipped, " ",
T_exporegm.exdose clipped, " ",
T_exporegm.exdoseunit clipped, " ",
T_exporegm.exroute, " given ",
T_exporegm.exinterval clipped, " x ",
T_exporegm.exduration[1,8] clipped
let hold_exserial = T_exporegm.exserial
end foreach
return hold_expo, hold_exserial
END FUNCTION
#####
FUNCTION show_fullcit(t_cit)
define
t_cit like citation.citnumb,
t_file like citation.citfile,
tmp_string char(75),
len, y, x smallint
call alrt1978open()
display "Preparing Citation Information ...." at 10, 10
attribute(reverse)
call disp_fullcit(t_cit)
menu "CURRENT PAPER"
command "Exit" HELP 1408
exit menu
end menu
call alrt1978close()
end function
#####
FUNCTION show_fullcit2(in_cit)
define
in_cit, t_cit like citation.citnumb
call alrt1978open()
display "Preparing Citation Information ...." at 4, 12
attribute(reverse)
declare full_cit2 scroll cursor for
select citnumb
from citation
where citnumb like in_cit
order by citnumb
open full_cit2
fetch first full_cit2 into t_cit
if status = NOTFOUND
THEN
MESSAGE "No papers found."
SLEEP 1
MESSAGE ""
```

```

RETURN
else
    call disp_fullcit(t_cit)
end if
menu "CURRENT-CITATIONS"
command "Next"
    "See next citation" HELP 1400
    fetch next full_cit2 into t_cit
    if status = NOTFOUND
        THEN
            MESSAGE "No more papers found in this direction."
            SLEEP 1
            MESSAGE ""
            fetch last full_cit2 into t_cit
            call disp_fullcit(t_cit)
        else
            call disp_fullcit(t_cit)
        end if
    command "Previous"
        "See Previous citation" HELP 1401
        fetch Previous full_cit2 into t_cit
        if status = NOTFOUND
            THEN
                MESSAGE "No more papers found in this direction."
                SLEEP 1
                MESSAGE ""
                fetch first full_cit2 into t_cit
                call disp_fullcit(t_cit)
            else
                call disp_fullcit(t_cit)
            end if
        command "Select"
            "Select the correct citation for use as is." HELP 1402
            let citnumber = t_cit
            select * into T_citation.*
            from citation
            where citnumb = t_cit
            call disntitle()
            call update_cit(t_cit)
            let sw = 0
        command "Use-Current"
            "Use the newly entered citation" HELP 1403
            exit menu
        command "Exit" HELP 2
            exit menu
        end menu
    call alert1978&close()
end function

*****
FUNCTION show_file(in_file)
define
    t_cit like citation.citnumb,
    t_journ like journal.jabrv,
    t_vol like citation.citvol,
    t_loc like citation.citlocat,
    t_page like citation.citpage,
    t_date like citation.citdate,

```

Toxin Knowledge System Source Code

```
t_title like citation.cititle,  
in_file, t_title like citation.citfile  
declare full_file2 search cursor for  
select citnumb from citation  
where citfile like in_file  
order by citnumb  
call airt1978open()  
display "Preparing Citation Information ...." at 4,12  
attribute(reverse)  
open full_file2  
fetch first full_file2 into t_cit  
if status = NOTFOUND  
THEN  
MESSAGE "No papers found."  
SLEEP 1  
MESSAGE ""  
RETURN  
else  
call disp_fullcit(t_cit)  
end if  
menu "CURRENT-CITATIONS"  
command "Next"  
"See next citation" HELP 1404  
fetch next full_file2 into t_cit  
if status = NOTFOUND  
THEN  
MESSAGE "No more papers found in this direction."  
SLEEP 1  
MESSAGE ""  
fetch last full_file2 into t_cit  
call disp_fullcit(t_cit)  
else  
call disp_fullcit(t_cit)  
end if  
command "Previous"  
"See Previous citation" HELP 1405  
fetch previous full_file2 into t_cit  
if status = NOTFOUND  
THEN  
MESSAGE "No more papers found in this direction."  
SLEEP 1  
MESSAGE ""  
fetch first full_file2 into t_cit  
call disp_fullcit(t_cit)  
else  
call disp_fullcit(t_cit)  
end if  
command "Select"  
"Select the correct citation for use as is." HELP 1406  
let citnumber = t_cit  
select * into T_citation *  
from citation  
where citnumb = t_cit  
call distitle()  
call update_cit(t_cit)  
let sw = 0  
command "Use-Current"
```

```

        "Use the newly entered citation." HELP 1407
    exit menu
    command "Exit" HELP 2
    exit menu
end menu
call alrt1978close()
end function
#####
FUNCTION disp_fullcit(t_cit)
define
    file_string char(80),
    t_file like citation.citfile,
    t_loc like citation.citlocate,
    t_cit like citation.citnumb,
    tmp_string char(800),
    y smallint
select citfile, citlocate into t_file, t_loc
from citation
where citnumb = t_cit
let file_string =
    "C#:", t_cit clipped, 3 spaces,
    "F#:", t_file clipped, 3 spaces,
    "Lc:", t_loc clipped
call biblio_gen(t_cit)
call keywd_list(t_cit)
display "" at 10,10
let y = 4
display file_string at 4,2
for x = 1 to length(bib_entry) step 75
    let y = y + 1
    let tmp_string = bib_entry(x, x+75)
    display tmp_string at y,2
end for
let y = y + 1
for x = 1 to length(keywdlst) step 75
    let y = y + 1
    let tmp_string = keywdlst(x, x+75)
    display tmp_string at y,2
end for
END FUNCTION

```

Pages 86 - 94 intentionally left blank

#tkspapovr.4gl

{Comments:

Title: tkspapovr.4gl

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University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Purpose: to manage the paper overview data

Contains the following functions:

```

    add_paper(pap_citnumb)
    find_paper(t_cit)
    view_paper()
    disp_paper(pap_citnumb)
    update_paper(pap_citnumb, tmp_papserial)
    alrt_dsgn_del(pap_citnumb)
    delete_paper(pap_citnumb, tmp_papserial)
    blowpaper(pap_citnumb, tmp_papserial)

```

}

database tkstest

GLOBALS "tksglob.4gl"

#####

FUNCTION add_paper(pap_citnumb)

define

```

    tmp_aim char(20),
    numdsgn, x smallint,
    pge integer,
    pap_citnumb like paperover.papcitnumb,
    aim char(1)

```

call papwinopen()

message ""

clear form

for x = 10 to 20

display "" at x. 1

end for

let pw = 0

options input wrap,

help file "t\shelp.msg",

help key F10

input by name

T_paperover.papcitnumb,

T_paperover.papcitfile,

T_paperover.papstatepur,

T_paperover.papimppur,

aim,

T_paperover.papaim,

T_paperover.papnumdsgn

on key(interrupt)

let pw = 1

exit input

before field papcitnu.nb

message "Hit RETURN to add data."

if pap_citnumb is not null

then

let T_paperover.papcitnumb = pap_citnumb

display by name T_paperover.papcitnumb

Toxin Knowledge System Source Code

```
        select citfile into citfileno
        from citation
        where citnumb = pap_citnumb
        let T_paperover.papcitfile = citfileno
        display by name T_paperover.papcitfile
        next field papstatepur
    end if
after field papcitnumb
    if T_paperover.papcitnumb is null
    then
        error "Must have CITATION number"
        next field papcitnumb
    else
        call exist_citnumb(T_paperover.papcitnumb) returning x
        if x = 0
        then
            error "No CITATION data has been entered for this number"
            next field papcitnumb
        else
            select count(*) into x from paperover
            where papcitnumb = T_paperover.papcitnumb
            if x > 0 then
                error beep, "PAPER OVERVIEW data already exists."
                next field papcitnumb
            end if
        end if
    end if
end if
select citfile into citfileno from citation
    where citnumb = T_paperover.papcitnumb
let T_paperover.papcitfile = citfileno
display by name T_paperover.papcitnumb
display by name T_paperover.papcitfile
message "Hit ESCAPE when enter data into database when finished."
next field papstatepur
before field aim
    if (T_paperover.papaim) is not null and aim <> "0"
    then
        let aim = T_paperover.papaim[1]
        message beep, "Enter 0 to see all Aim Choices"
        attrib (reverse)
    else
        let aim = "0"
    end if
    call aim_choice(aim)
after field aim
    if aim = "0"
    then
        next field aim
    else
        call aim_choice(aim)
        if chosen = 0
        then next field aim
        end if
        message "Hit ESC to add row"
    end if
after field papaim
    call aim_trans(T_paperover.papaim) returning tmp_aim
```

```

    if chosen = 0
        then next field papaim
    end if
    display tmp_aim to class
    call clear_choice(8,16,50)
before field papnumdsgn
    call show_dsgn(T_paperover.papcitnumb, 0) returning pge
    on key (control-P)
        if infield(egdsgn) then
            call show_dsgn(T_paperover.papcitnumb, pge-1) returning pge
        end if
    on key (CONTROL-N)
        if infield(egdsgn) then
            call show_dsgn(T_paperover.papcitnumb, pge+1) returning pge
        end if
after field papnumdsgn
    let numdsgn = T_paperover.papnumdsgn
    if T_paperover.papaim[1] = "I"
        then
            if (numdsgn <> 0 or cnt <> 0) then
                Error "Cannot have designs for information only papers"
                next field aim
            end if
        else
            if numdsgn = 0 then
                Error beep, "Design Required for this paper aim"
                next field aim
            end if
        end if
    On key (control-w)
        case
            when infield(papstatepur)
                call showhelp(400)
            when infield(papimppur)
                call showhelp(401)
            when infield(papaim)
                call showhelp(402)
            when infield(papnumdsgn)
                call showhelp(403)
        end case
    after input
        let T_paperover.papserial = 0
    end input
options help key control-w
if pw = 1 then return end if
insert into paperover values(T_paperover.*)
message "Row Added"
sleep 1
message ""
select count(*) into x from stdydsgn
where stycitnumb = T_paperover.papcitnumb
if status = NOTFOUND
    then let x = 0
end if
call papwinclose()
if T_paperover.papnumdsgn > x
    then call add_dsgn(pap_citnumb, T_paperover.papnumdsgn, x)

```


Toxin Knowledge System Source Code

```
    end if
  END FUNCTION
#####
FUNCTION find_paper(t_cit)
  define
    t_cit like paperover.papcitnumb
  call papwinopen()
  case
    when t_cit is null
      clear form
      message "Enter search criteria and hit ESC to search"
      let int_flag=0
      construct by name query1 on paperover.*
      if int_flag <> 0 then return end if
      let select1 = "select * from paperover where ",
        query1 clipped, " order by papcitnumb"
      let select2 = "select count(*) from paperover where ",
        query1 clipped
      exit case
    otherwise
      let select1="select * from paperover where papcitnumb = ",
        quote, t_cit clipped, quote, " order by papcitnumb"
      let select2="select count(*) from paperover where papcitnumb = ",
        quote, t_cit clipped, quote
      exit case
    end case
  prepare select_paper from select1
  prepare cnt_paper from select2
  declare cnt_curs cursor for cnt_paper
  foreach cnt_curs into cnt
    end foreach
  declare p_curs scroll cursor for select_paper
  open p_curs
  call view_paper()
  close p_curs
  call papwinclose()
END FUNCTION
#####
FUNCTION view_paper()
  fetch first p_curs into T_paperover.*
  if status = NOTFOUND
    then
      MESSAGE "No papers found."
      SLEEP 1
      MESSAGE ""
    else
      let tmp_cnt = 1
      call disp_paper(T_paperover.papcitnumb)
      display "" at 21,2
      display " ", tmp_cnt, " of ", cnt, " rows found." at 21,2
    end if
  end if
MENU "BROWSE"
  COMMAND "Next" "View the next Paper in the list." HELP 170
  FETCH NEXT p_curs INTO T_paperover.*
  let tmp_cnt = tmp_cnt + 1
  IF status = NOTFOUND THEN
    MESSAGE "No more Papers in this direction."
```

```

        SLEEP 1
        let tmp_cnt = cnt
        MESSAGE ""
        FETCH LAST p_curs INTO T_paperover.*
        END IF
    display "" at 21,2
    display " ",tmp_cnt," of ", cnt," rows" at 21,2
        attribute(reverse)
    call disp_paper(T_paperover.papcitnumb)
COMMAND "Previous" "View the Previous Paper in the list." HELP 170
    FETCH PREVIOUS p_curs INTO T_paperover.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
        MESSAGE "No more Papers in this direction."
        SLEEP 1
        MESSAGE ""
        let tmp_cnt = 1
        FETCH FIRST p_curs INTO T_paperover.*
        END IF
    display "" at 21,2
    display " ",tmp_cnt," of ", cnt," rows" at 21,2
        attribute(reverse)
    call disp_paper(T_paperover.papcitnumb)
COMMAND "First" "View the first Paper in the list." HELP 170
    FETCH FIRST p_curs INTO T_paperover.*
    let tmp_cnt = 1
    display "" at 21,2
    display " ",tmp_cnt," of ", cnt," rows" at 21,2
        attribute(reverse)
    call disp_paper(T_paperover.papcitnumb)
COMMAND "Last" "View the Last Paper in the list" HELP 170
    message "Searching for last record...."
    FETCH LAST p_curs INTO T_paperover.*
    let tmp_cnt = cnt
    message ""
    display "" at 21,2
    display " ",tmp_cnt," of ", cnt," rows" at 21,2
        attribute(reverse)
    call disp_paper(T_paperover.papcitnumb)
COMMAND "Update" "Update data in this paper" HELP 171
    call update_paper(T_paperover.papcitnumb,
        T_paperover.papsenal)
COMMAND "Delete" "Delete this entry from database" HELP 404
    call delete_paper(T_paperover.papcitnumb,
        T_paperover.papsenal)
COMMAND "Query-Again" "Enter new search criteria"
    close p_curs
    let citnumber = ""
    call find_paper(citnumber)
    exit menu
COMMAND "Exit" "Leave this menu" HELP 2
    EXIT MENU
END MENU
END FUNCTION
=====
FUNCTION disp_paper(pap_citnumb)
    define

```

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```
tmp_aim char(20),
pap_citnumb like paperover.papcitnumb,
x smallint
for x = 10 to 20
  display "" at x, 1
end for
display by name T_paperover.*
call aim_trans(T_paperover.papaim) returning tmp_aim
display tmp_aim to class
call show_dsgn(T_paperover.papcitnumb, 0) returning x
END FUNCTION
#####
FUNCTION update_paper(pap_citnumb, tmp_papserial)
define
  tmp_aim char(20),
  pap_citnumb, tmp_citno like paperover.papcitnumb,
  pge, tmp_papserial integer,
  aim cvar(1),
  numdsgn, hold_dsgn, x, pw smallint
message ""
let tmp_citno = pap_citnumb
let pw = 0
message "Hit ESC to update row."
input by name
  T_paperover.papcitnumb,
  T_paperover.papcitfile,
  T_paperover.papstatepur,
  T_paperover.papimppur,
  aim,
  T_paperover.papaim,
  T_paperover.papnumdsgn
without defaults
on key(interrupt)
  let pw = 1
  exit input

after field papcitnumb
  message "Hit ESCAPE to update row"
  if T_paperover.papcitnumb is null
    then error "Must have citnumber!"
  end if
  if pap_citnumb <> T_paperover.papcitnumb
    then call exist_citnumb(T_paperover.papcitnumb) returning x
    if x = 0
      then
        error beep, "No CITATION entered with this NUMBER "
        next field papcitnumb
      else
        select count(*) into x from paperover
          where papcitnumb = T_paperover.papcitnumb
        if x > 0 then
          error "PAPER data already entered for this paper."
          sleep 2
          next field papcitnumb
        end if
      end if
    end if
  end if
end if
```

```

before field aim
  if (T_paperover.papaim) is not null and aim <> "0"
    then
      let aim = T_paperover.papaim[1]
      message beep, "Enter 0 to see all Aim Choices"
      attribute (reverse)
    else
      let aim = "0"
    end if
  call aim_choice(aim)
after field aim
  if aim = "0"
    then
      next field aim
    else
      call aim_choice(aim)
      if chosen = 0
        then next field aim
      end if
      message "Hit ESC to update row"
    end if
after field papaim
  call aim_trans(T_paperover.papaim) returning tmp_aim
  if chosen = 0
    then next field papaim
  end if
  display tmp_aim to class
  call clear_choice(8,16,50)
before field papnumdsgn
  call show_dsgn(T_paperover.papcitnumb, 0) returning pge
  on key (control-P)
    if infield(egdsgn) then
      call show_dsgn(T_paperover.papcitnumb, pge-1) returning pge
    end if
  on key (CONTROL-N)
    if infield(egdsgn) then
      call show_dsgn(T_paperover.papcitnumb, pge+1) returning pge
    end if
after field papnumdsgn
  select count(*) into hold_dsgn
  from stdydsgn
  where stycitnumb = T_paperover.papcitnumb
  if status = NOTFOUND then
    let hold_dsgn = 0
  end if
  let numdsgn = T_paperover.papnumdsgn
  if T_paperover.papaim[1] = "1"
    then
      if (numdsgn <> 0 or hold_dsgn <> 0)
        then
          Error "Cannot have designs for information only papers"
          next field aim
        end if
      else
        Case
        when numdsgn = 0
          Error beep, "Design Required for this paper aim"

```

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```
        next field aim
        exit case
    when hold_dsgn < T_paperover.papnumdsgn
        call add_dsgn(T_paperover.papcitnumb, T_paperover.papnumdsgn, 0)
        call add_exgp(T_paperover.papcitnumb)
        exit case
    when hold_dsgn > T_paperover.papnumdsgn
        call alrt_dsgn_del(T_paperover.papcitnumb)
        exit case
    end case
end if
end input
if pw = 1 then return end if
update paperover set paperover.* = T_paperover.*
    where papserial = tmp_papserial
if tmp_citno <> T_paperover.papcitnumb
    then
        UPDATE stdydsgn
            set stycitnumb = T_paperover.papcitnumb,
            stycitfile = T_paperover.papcitfile
            where stycitnumb = tmp_citno
        UPDATE subigrp
            set sgcitnumb = T_paperover.papcitnumb
            where sgcitnumb = tmp_citno
        UPDATE exporegm
            set excitnumb = T_paperover.papcitnumb
            where excitnumb = tmp_citno
        UPDATE expogrp
            set egcitnumb = T_paperover.papcitnumb
            where egcitnumb = tmp_citno
        UPDATE clinfiad
            set cfcitnumb = T_paperover.papcitnumb
            where cfcitnumb = tmp_citno
        UPDATE tksccomment
            set cocitnumb = T_paperover.papcitnumb,
            cocitfile = T_paperover.papcitfile
            where cocitnumb = tmp_citno
    end if
    message "Row updated!"
    sleep 1
END FUNCTION
#####
FUNCTION alrt_dsgn_del(pap_citnumb)
    define
        pap_citnumb like paperover.papcitnumb,
        hold_dsgncur integer,
        hold_dsgnserial integer
    call alrt265open()
    menu "There are more designs than indicated"
        COMMAND "Cancel" "Return and correct number of designs" HELP 405
        exit menu
        COMMAND "Delete-Design" "Search for and delete designs" HELP 406
        Prompt "Which of displayed designs should be deleted? > "
        for hold_dsgncur HELP 411
        select styserial into hold_dsgnserial from stdydsgn
            where stydsgncur = hold_dsgncur
            and stycitnum = pap_citnumb
```

```

        call delete_dsign(pap_citnumb,hold_dsgnserial)
    end menu
    call alrt265close()
END FUNCTION
#####
FUNCTION delete_paper(pap_citnumb, tmp_papserial)
    define
        pap_citnumb like paperover.papcitnumb,
        tmp_papserial integer
    prompt "Do you want to delete this paper overview? (y/n)"
    for answer
    IF upshift(answer) = "N"
    then
        MESSAGE "Row NOT deleted."
        sleep 1
        MESSAGE ""
        RETURN
    else
        select stycitnumb from stdydsgn
            where stycitnumb = pap_citnumb
        union
        select excitnumb from exporegm
            where excitnumb = pap_citnumb
        union
        select sgcitnumb from subjgrp
            where sgcitnumb = pap_citnumb
        union
        select egcitnumb from expogrp
            where egcitnumb = pap_citnumb
        union
        select cfcitnumb from clinfind
            where cfcitnumb = pap_citnumb
        if status = NOTFOUND
        then
            DELETE FROM paperover
                where papserial = tmp_papserial
            MESSAGE "Row deleted."
            SLEEP 1
            MESSAGE ""
        else
            call blowpaper(pap_citnumb,tmp_papserial)
        end if
    end if
END FUNCTION
#####
FUNCTION blowpaper(pap_citnumb,tmp_papserial)
    define
        pap_citnumb like paperover.papcitnumb,
        tmp_papserial integer,
        hold_dsgn smallint,
        hold_msg char(80)
    call alrt270open()
    message beep, beep, beep, "There are other tables linked to this record"
    sleep 2
    menu "DELETE_PAPER"
        COMMAND "Exit"    HELP 2
    exit menu

```

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```
COMMAND "All-Links"  
  "Delete all linked paper-related tables.CAN BE DANGEROUS"      HELP 408  
  menu "DO YOU REALLY WANT TO DELETE ALL CONNECTED TABLES ? "  
    COMMAND "No"  HELP 409  
    exit menu  
    COMMAND "Yes"  HELP 410  
    delete from paperver  
      where papserial = tmp_papserial  
    select count(*) into hold_dsgn from stdydsgn  
      where stycitnumb = pap_citnumb  
    display "" at 2,2  
    display " ", hold_dsgn using "<<&",  
      " designs deleted" at 2,2  
    delete from stdydsgn where stycitnumb = pap_citnumb  
    select count(*) into hold_dsgn from exporegm  
      where excitnumb = pap_citnumb  
    display "" at 2,2  
    display " ", hold_dsgn using "<<&",  
      " exposure regimens deleted" at 2,2  
    delete from exporegm  
      where excitnumb = pap_citnumb  
    select count(*) into hold_dsgn from subjgrp  
      where sgcitnumb = pap_citnumb  
    display "" at 2,2  
    display " ", hold_dsgn using "<<&",  
      " subject groups deleted" at 2,2  
    delete from subjgrp  
      where sgcitnumb = pap_citnumb  
    select count(*) into hold_dsgn from expogrp  
      where egcitnumb = pap_citnumb  
    display "" at 2,2  
    display " ", hold_dsgn using "<<&",  
      " exposure groups deleted" at 2,2  
    delete from expogrp  
      where egcitnumb = pap_citnumb  
    select count(*) into hold_dsgn from clinfind  
      where cfcitnumb = pap_citnumb  
    display "" at 2,2  
    display " ", hold_dsgn using "<<&",  
      " clinical findings deleted" at 2,2  
    delete from clinfind  
      where cfcitnumb = pap_citnumb  
    exit menu  
  end menu  
exit menu  
end menu  
call airt2:fclose()  
END FUNCTION
```

#tksdsgn.4gl

```

(
Title: tksdsgn.4gl
Copyright Harold L. Trammel, 1987-1988
University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
Contains the following functions:
    add_dsgn(tmp_stycitnumb, tot_numdsgn, dsgnnum_cnt)
    find_dsgn(t_cit)
    view_design()
    disp_dsgn(tmp_stycitnumb, tmp_styserial)
    update_dsgn(tmp_stycitnumb, tmp_styserial)
    delete_design(tmp_stycitnumb, tmp_styserial)
    blowdesign(tmp_stycitnumb, tmp_styserial)
    renum_dsgn(tmp_stycitnumb, del_dsgn, tot_dsgn)
    add_details(t_cit, t_type, t_subj, t_expo, t_dsgn)
    chk_cntl_chnge()
    alrt_box1()
    alrt_box2()
)
database tkstest
globals "tksglob.4gl"
#####
FUNCTION add_dsgn(t_stycitnumb, tot_numdsgn, dsgnnum_cnt)
    # citation number, total number of designs, existing number of designs
    define
        stdy_trans char(20),
        vivvit char(10),
        study, cntlcmp, cntltyp, cntlmeth char(20),
        compmeth, cntlassgn char(20),
        tot_numdsgn, hold_dsgn like stdydsgn.stydsgr.tot,
        numsubj like stdydsgn.stynumgrp,
        numexpo like stdydsgn.stynumexp,
        tmp_aim like paperover.papaim,
        tmp_2ch char(2),
        t_stycitnumb, tmp_cit like stdydsgn.stycitnumb,
        dsgn_cnt, dsgnnum_cnt smallint,
        tmp_styserial integer,
        y, z smallint
    # initial setup
    call dsgnwinopen()
    clear form
    let dw = 0
    select papaim into tmp_aim from paperover
        where papcitnumb = t_stycitnumb
    for cnt = (dsgnnum_cnt+1) to tot_numdsgn
        initialize dsgn_array[cnt].* to null
    end for
    call set_count(tot_numdsgn)
    options help file "tkshelp.msg"
    select citfile into citfileno
        from citation
        where citnumb = t_stycitnumb
    input array dsgn_array from dsgn_rec.*
    on key(interrupt)
        let dw = 1

```


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```
exit input
ON Key(control-w)
case
  when infield(stycitnumb)
    call showhelp(500)
  when infield(stycitfile)
    call showhelp(517)
  when infield(dsgncur)
    call showhelp(518)
  when infield(dsgntot)
    call showhelp(519)
  when infield(styvivit)
    call showhelp(501)
  when infield(stycntl)
    call showhelp(503)
  when infield(stycntlcmp)
    call showhelp(504)
  when infield(stycmpmeth)
    call showhelp(505)
  when infield(stycntlmeth)
    call showhelp(506)
  when infield(stycntltyp)
    call showhelp(507)
  when infield(stycntassgn)
    call showhelp(508)
  when infield(numsubj)
    call showhelp(509)
  when infield(stynumexp)
    call showhelp(510)
end case

before field stycitnumb
let curr_arr = arr_curr() + dsgnum_cnt
let dsgn_cnt = arr_count() + dsgnum_cnt
let dsgn_array[curr_arr].styserial = 0
let dsgn_array[curr_arr].stydsgncur = curr_arr
let hold_dsgn = curr_arr
let dsgn_array[curr_arr].stydsgntot = dsgn_cnt
#initial displays
  message "Hit RETURN to begin to add data."
  display "" to study
  display "" to vivvit
  display "" to cntlcmp
  display "" to compmeth
  display "" to cntlmeth
  display "" to cntltyp
  display "" to cntlassgn
  display by name dsgn_array[curr_arr].stydsgncur
  display by name dsgn_array[curr_arr].stydsgntot
if t_stycitnumb is not null
  then
    let dsgn_array[curr_arr].stycitnumb = t_stycitnumb
    let dsgn_array[curr_arr].stycitfile = citfileno
    display by name dsgn_array[curr_arr].stycitnumb
    display by name dsgn_array[curr_arr].stycitfile
  next field stytype
```

```

        end if
    after field stycitnumb
        if dsgn_array[curr_arr].stycitnumb is null
            then
                error "Must have Citation Number"
            next field stycitnumb
        else
            let tmp_cit = dsgn_array[curr_arr].stycitnumb
            let x = exist_citnumb( tmp_cit)
            if x = 0 then
                error "No CITATION DATA entered with this number."
            next field stycitnumb
            end if
        end if
    let dsgn_array[curr_arr].stycitnumb = t_stycitnumb
    let dsgn_array[curr_arr].stycitfile = citfileno
    display by name dsgn_array[curr_arr].stycitnumb
    display by name dsgn_array[curr_arr].stycitfile
    next field stytype
before field stytype
    call stype_choice(tmp_aim)
after field stytype
    let tmp_2ch = dsgn_array[curr_arr].stytype
    call stype_trans(tmp_2ch) returning study
    display by name study
before field styvivit
    call vivit_choice()
after field styvivit
    let tmp_2ch = dsgn_array[curr_arr].styvivit
    call vivit_trans(tmp_2ch) returning vivvit
    if chosen = 0
        then next field styvivit
    else display by name vivvit
    end if
before field stycntl
    if dsgn_array[curr_arr].stytype = "F"
        then let dsgn_array[curr_arr].stycntl = "N"
    next field stynumgrp
    end if
after field stycntl
    if dsgn_array[curr_arr].stycntl = "N"
        then
            let dsgn_array[curr_arr].stycntlcmp = ""
            let dsgn_array[curr_arr].stycmpmeth = ""
            let dsgn_array[curr_arr].stycntlmeth = ""
            let dsgn_array[curr_arr].stycntltyp = ""
            let dsgn_array[curr_arr].stycntassgn = ""
            display by name dsgn_array[curr_arr].stycntlcmp
            display by name dsgn_array[curr_arr].stycmpmeth
            display by name dsgn_array[curr_arr].stycntlmeth
            display by name dsgn_array[curr_arr].stycntltyp
            display by name dsgn_array[curr_arr].stycntassgn
            next field stynumgrp
        end if
before field stycntlcmp
    if dsgn_array[curr_arr].stycntl = "N"
        then next field stycntl

```

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```
        else call cntlcmp_choice()
        end if
    after field stycntlcmp
        let tmp_2ch = dsgn_array[curr_arr].stycntlcmp
        call cntlcmp_trans(tmp_2ch) returning cntlcmp
        if chosen = 0
            then next field stycntlcmp
            else display by name cntlcmp
            end if
    before field stycmpmeth
        let tmp_2ch = dsgn_array[curr_arr].stycntlcmp
        call cmpmeth_choice(tmp_2ch)
    after field stycmpmeth
        let tmp_2ch = dsgn_array[curr_arr].stycmpmeth
        call cmpmeth_trans(tmp_2ch) returning compmeth
        if chosen = 0
            then next field stycmpmeth
            else display by name cornpmeth
            end if
    before field stycntlmeth
        if dsgn_array[curr_arr].stycntl = "N"
            then next field stycntl
            else call cntlmeth_choice()
            end if
    after field stycntlmeth
        let tmp_2ch = dsgn_array[curr_arr].stycntlmeth
        call cntlmeth_trans(tmp_2ch) returning cntlmeth
        if chosen = 0
            then next field stycntlmeth
            else display by name cntlmeth
            end if
    before field stycntltyp
        let tmp_2ch = dsgn_array[curr_arr].stycntlmeth
        call cntltyp_choice(tmp_2ch)
    after field stycntltyp
        let tmp_2ch = dsgn_array[curr_arr].stycntltyp
        call cntltyp_trans(tmp_2ch) returning cntltyp
        if chosen = 0
            then next field stycntltyp
            else display by name cntltyp
            end if
    before field stycntassgn
        call cntlassgn_choice()
    after field stycntassgn
        let tmp_2ch = dsgn_array[curr_arr].stycntassgn
        call cntlassgn_trans(tmp_2ch) returning cntlassgn
        if chosen = 0
            then next field stycntassgn
            else display by name cntlassgn
            end if
    after field stynumgrp
        let numsubj = dsgn_array[curr_arr].stynumgrp
        if numsubj > 99
            then
                error beep, "The maximum number of Subject Groups is 99!"
            next field stynumgrp
            end if
```

```

call add_details(t_stycitnumb,study,numsubj,0,hold_dsgn)
select count(*) into cnt from subjgrp
  where sgcitnumb = dsgn_array[curr_arr].stycitnumb
  and sgdsgnnum = dsgn_array[curr_arr].stydsngcur
display cnt using "<<&", "Groups Entered " at 19,40
  attribute(reverse)
after field stynumexp
  let numexpo = dsgn_array[curr_arr].stynumexp
  if numexpo > 99
    then
      error beep, "The maximum number of Exposure Regimens is 99!"
    next field stynumexp
  end if
call add_details(t_stycitnumb,study,0,numexpo,hold_dsgn)
select count(*) into cnt from exporegm
  where excitnumb = dsgn_array[curr_arr].stycitnumb
  and exdsgnnum = dsgn_array[curr_arr].stydsngcur
display cnt using "<<&", "Regimens Entered " at 20,40
  attribute(reverse)
if dsgn_cnt = tot_numdsgn
  then exit input
end if
end input
if dw = 1 then return end if
for cnt = (dsgnnum_cnt+1) to dsgn_cnt
  insert into stdydsgn values(
    dsgn_array[cnt].stycitnumb,
    dsgn_array[cnt].stycitfile,
    dsgn_array[cnt].styserial,
    dsgn_array[cnt].stydsngcur,
    dsgn_cnt,
    dsgn_array[cnt].stytype,
    dsgn_array[cnt].styvivit,
    dsgn_array[cnt].stycntl,
    dsgn_array[cnt].stycntlcmp,
    dsgn_array[cnt].stycmpmeth,
    dsgn_array[cnt].stycntlmeth,
    dsgn_array[cnt].stycntltyp,
    dsgn_array[cnt].stycntassgn,
    dsgn_array[cnt].stynumgrp,
    dsgn_array[cnt].stynumexp)

#converts temporary dsgn number to serial number in subj and expo
select styserial into tmp_styserial
  from stdydsgn
  where stycitnumb = dsgn_array[cnt].stycitnumb
  and stydsngcur = dsgn_array[cnt].stydsngcur
update exporegm
  set exdsgnnum = tmp_styserial
  where excitnumb = dsgn_array[cnt].stycitnumb
  and exdsgnnum = dsgn_array[cnt].stydsngcur
update subjgrp
  set sgdsgnnum = tmp_styserial
  where sgcitnumb = dsgn_array[cnt].stycitnumb
  and sgdsgnnum = dsgn_array[cnt].stydsngcur
end for
call swinclose()

```

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```
call expwinclose()
call dsgnwinclose()
END FUNCTION
#####
FUNCTION find_dsgn(t_cit)
define t_cit like stdydsgn.stycitnumb
call dsgnwinopen()
case
    when t_cit is null
        clear form
        message "Enter search criteria and hit ESC to begin search"
        let int_flag=0
        construct by name query1 on stdydsgn.*
        if int_flag <> 0 then return end if
        let select1 = "select * from stdydsgn where ",
            query1 clipped, " order by stycitnumb, stydsgncur"
        let select2 = "select count(*) from stdydsgn where ",
            query1 clipped
        exit case
    otherwise
        let select1 = "select * from stdydsgn where ",
            "stycitnumb = ", quote, t_cit, quote,
            " order by stycitnumb, stydsgncur"
        let select2 = "select count(*) from stdydsgn where ",
            "stycitnumb = ", quote, t_cit, quote
        exit case
    end case
prepare select_design from select1
prepare cnt_design from select2
display "Searching . . ." at 21,2 attribute(reverse)
declare cnt_curs cursor for cnt_design
foreach cnt_curs into cnt
end foreach
declare d_curs scroll cursor for select_design
open d_curs
call view_design()
close d_curs
END FUNCTION
#####
FUNCTION view_design()
fetch first d_curs into T_stdydsgn.*
if status = NOTFOUND
then
    MESSAGE "No designs found.", beep
    SLEEP 1
    MESSAGE ""
    display "" at 21,2
else
    let tmp_cnt = 1
    display "" at 21,2
    call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
    display " ", tmp_cnt, " of ", cnt, " rows found." at 21,2
end if
MENU "BROWSE"
COMMAND "Next"
    "View the next Design in the list." HELP 170
FETCH NEXT d_curs INTO T_stdydsgn.*
```

```

let tmp_cnt = tmp_cnt + 1
IF status = NOTFOUND THEN
    MESSAGE "No more Designs in this direction."
    SLEEP 1
    let tmp_cnt = cnt
    MESSAGE ""
    FETCH LAST d_curs INTO T_stdydsgn.*
    END IF
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
attribute(reverse)
call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
COMMAND "Previous"
"View the Previous Design in the list." HELP 170
FETCH PREVIOUS d_curs INTO T_stdydsgn.*
let tmp_cnt = tmp_cnt - 1
IF status = NOTFOUND THEN
    MESSAGE "No more Designs in this direction."
    SLEEP 1
    MESSAGE ""
    let tmp_cnt = 1
    FETCH FIRST d_curs INTO T_stdydsgn.*
    END IF
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
attribute(reverse)
call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
COMMAND "First"
"View the first Design in the list." HELP 170
FETCH FIRST d_curs INTO T_stdydsgn.*
let tmp_cnt = 1
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
attribute(reverse)
call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
COMMAND "Last"
"View the Last Design in the list." HELP 170
message "Searching for last record...."
FETCH LAST d_curs INTO T_stdydsgn.*
let tmp_cnt = cnt
message ""
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
attribute(reverse)
call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
COMMAND "Update"
"Update the Current Design in the list." HELP 171
call update_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
COMMAND "Delete"
"Delete this entry from database" HELP 511
call delete_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)
call disp_dsgn(T_stdydsgn.stycitnumb,T_stdydsgn.styserial)

COMMAND "Query-Again"
"Enter new search criteria" HELP 512
close d_curs

```

Toxin Knowledge System Source Code

```
    let citnumber = ""
    call find_dsgn(citnumber)
    exit menu
COMMAND "Exit"
    "Leave this menu:" HELP 2
    close d_curs
    EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION disp_dsgn(tmp_stycitnumb, tmp_styserial)
    define stdy_trans char(20),
        vivvit char(10),
        study, cntlcmp, cntltyp, cntlmeth, compmeth, cntlassgn char(20),
        tmp_stycitnumb like stdydsgn.stycitnumb,
        tmp_numdsgn like stdydsgn.stydsgntot,
        tmp_styserial integer,
        tmp_grp,tmp_exp smallint
    display by name T_stydsgn.*
    if T_stydsgn.stytype is not null
        then call stype_trans(T_stydsgn.stytype) returning study
        else let study = ""
        end if
    display by name study
    if T_stydsgn.styvivit is not null
        then call vivit_trans(T_stydsgn.styvivit) returning vivvit
        else let vivvit = ""
        end if
    display by name vivvit
    if T_stydsgn.stycntlcmp is not null
        then call cntlcmp_trans(T_stydsgn.stycntlcmp) returning cntlcmp
        else let cntlcmp = ""
        end if
    display by name cntlcmp
    if T_stydsgn.stycmpmeth is not null
        then call cmpmeth_trans(T_stydsgn.stycmpmeth) returning compmeth
        else let compmeth = ""
        end if
    display by name compmeth
    if T_stydsgn.stycntlmeth is not null
        then call cntlmeth_trans(T_stydsgn.stycntlmeth) returning cntlmeth
        else let cntlmeth = ""
        end if
    display by name cntlmeth
    if T_stydsgn.stycntltyp is not null
        then call cntltyp_trans(T_stydsgn.stycntltyp) returning cntltyp
        else let cntltyp = ""
        end if
    display by name cntltyp
    if T_stydsgn.stycntassgn is not null
        then call cntlassgn_trans(T_stydsgn.stycntassgn) returning cntlassgn
        else let cntlassgn = ""
        end if
    display by name cntlassgn
    select count(*) into tmp_grp
    from subigrp
    where sgcitnumb = tmp_stycitnumb
```

```

and sgdsnum = tmp_styserial
display tmp_grp using "<<&", " Groups Entered " at 19,40
attribute(reverse)
select count(*) into tmp_exp
from exporegm
where excitnumb = tmp_stycitnumb
and exdsnum = tmp_styserial
display tmp_exp using "<<&", " Regimens Entered " at 20,40
attribute(reverse)
END FUNCTION
#####
FUNCTION update_dsgn(tmp_stycitnumb, tmp_styserial)
define stdy_trans char(20),
vivot char(10),
study, cntlcmp, cntltyp, cntlmeth, compmeth, cntlassgn char(20),
tmp_stycitnumb like stdydsgn.stycitnumb,
tmp_numdsgn, numdsgn like stdydsgn.stydsgntot,
numsubj like stdydsgn.stynumgrp,
numexpo like stdydsgn.stynumexp,
tmp_aim like paperover.papaim,
tmp_styserial integer,
sg_cnt, ex_cnt, y, z smallint
let dw = 0
let tmp_numdsgn = T_stdydsgn.stydsgncur
select papaim into tmp_aim from paperover
where papcitnumb = T_stdydsgn.stycitnumb
options input wrap,
help file "tkshelp.msg"
input T_stdydsgn.* without defaults from dsgn_rec.*
on key(interrupt)
let dw = 1
exit input
ON Key(control-w)
case
when infield(stycitnumb)
call showhelp(500)
when infield(stycitfile)
call showhelp(517)
when infield(dsgncur)
call showhelp(518)
when infield(dsgntot)
call showhelp(519)
when infield(styvivot)
call showhelp(501)
when infield(stycntl)
call showhelp(503)
when infield(stycntlcmp)
call showhelp(504)
when infield(stycmpmeth)
call showhelp(505)
when infield(stycntlmeth)
call showhelp(506)
when infield(stycntltyp)
call showhelp(507)
when infield(stycntassign)
call showhelp(508)
when infield(numsubj)

```


Toxin Knowledge System Source Code

```
        call showhelp(509)
        when infield(stynumexp)
            call showhelp(510)
        end case

before field stycitnumb
    message "Hit ESC to update row"
after field stycitnumb
    if T_stdydsgn.stycitnumb is null
        then
            error "You must have a CITATION number"
            next field stycitnumb
        end if
    if T_stdydsgn.stycitnumb <> tmp_stycitnumb
        then
            call exist_citnumb(T_stdydsgn.stycitnumb) returning x
            if x = 0
                then
                    error "CITATION data not entered for this number"
                    next field stycitnumb
                else
                    select count(*) into x
                    from stdydsgn
                    where stycitnumb = T_stdydsgn.stycitnumb
                    if x > 0
                        then
                            error "DESIGN data already entered for this number"
                            next field stycitnumb
                        end if
                    end if
                end if
            end if
        next field stytype
    after field stydsgncur
        if T_stdydsgn.stydsgncur <> tmp_numdsgn
            then
                select count(*) into x from stdydsgn
                where stydsgncur = T_stdydsgn.stydsgncur
                and stycitnumb = T_stdydsgn.stycitnumb
                if x > 0 then
                    error "Data already entered for that Design Number"
                    next field stydsgncur
                end if
            end if
        before field stytype
            call stype_choice(tmp_aim)
        after field stytype
            call stype_trans(T_stdydsgn.stytype) returning study
            display by name study
        before field styvivit
            call vivit_choice()
        after field styvivit
            call vivit_trans(T_stdydsgn.styvivit) returning vivvit
            if chosen = 0
                then next field styvivit
            else display by name vivvit
            end if
    after field stycnt1
```

```

if T_stdydsgn.stycntl = "N"
  then
    let T_stdvdsgn.stycntlcmp = ""
    let T_stdydsgn.stycmpmeth = ""
    let T_stdydsgn.stycntlmeth = ""
    let T_stdydsgn.stycntltyp = ""
    let T_stdydsgn.stycntassgn = ""
    display by name T_stdydsgn.stycntlcmp
    display by name T_stdydsgn.stycmpmeth
    display by name T_stdydsgn.stycntlmeth
    display by name T_stdydsgn.stycntltyp
    display by name T_stdydsgn.stycntassgn
    next field stynumgrp
  end if
before field stycntlcmp
  if T_stdydsgn.stycntl = "N"
    then next field stycntl
    else call cntlcmp_choice()
  end if
after field stycntlcmp
  call cntlcmp_trans(T_stdydsgn.stycntlcmp) returning cntlcmp
  if chosen = 0
    then next field stycntlcmp
    else display by name cntlcmp
  end if
before field stycmpmeth
  call cmpmeth_choice(T_stdydsgn.stycntlcmp)
after field stycmpmeth
  call cmpmeth_trans(T_stdydsgn.stycmpmeth) returning compmeth
  if chosen = 0
    then next field stycmpmeth
    else display by name compmeth
  end if
before field stycntlmeth
  if T_stdydsgn.stycntl = "N"
    then next field stycntl
    else call cntlmeth_choice()
  end if
after field stycntlmeth
  call cntlmeth_trans(T_stdydsgn.stycntlmeth)
  returning cntlmeth
  if chosen = 0
    then next field stycntlmeth
    else display by name cntlmeth
  end if
before field stycntltyp
  call cntltyp_choice(T_stdydsgn.stycntlmeth)
after field stycntltyp
  call cntltyp_trans(T_stdydsgn.stycntltyp)
  returning cntltyp
  if chosen = 0
    then next field stycntltyp
    else display by name cntltyp
  end if
before field stycntassgn
  call cntlassgn_choice()
after field stycntassgn

```

Toxia Knowledge System Source Code

```

call cntlassgn_trans(T_stdydsgn.stycntassgn)
returning cntlassgn
if chosen = 0
    then next field stycntassgn
    else display by name cntlassgn
end if
before field stynumgrp
let numsubj = T_stdydsgn.stynumgrp
select count(*) into x
from subjgrp
where sgcitnumb = T_stdydsgn.stycitnumb
and sgdsgnnum = T_stdydsgn.stydsngcur
after field stynumgrp
if T_stdydsgn.stynumgrp > 99
    then error beep, "The maximum number of Subject Groups is 99!"
    next field stynumgrp
end if
case
when x = T_stdydsgn.stynumgrp
    next field stynumexp
exit case
when x < T_stdydsgn.stynumgrp
    call add_details(T_stdydsgn.stycitnumb,
        T_stdydsgn.stytype,
        T_stdydsgn.stynumgrp,
        0,
        T_stdydsgn.styserial)
    select count(*) into sg_cnt
    from subjgrp
    where sgcitnumb = T_stdydsgn.stycitnumb
    and sgdsgnnum = T_stdydsgn.styserial
    let T_stdydsgn.stynumgrp = sg_cnt
    display sg_cnt using "<<&", " Groups Entered" " at 19,40 attribute(reverse)
    # needs flag to force jump to exposure groups
exit case
when numsubj < T_stdydsgn.stynumgrp
    call alrt_box1()
    if upshift(answer) = "Y"
        then
            call add_details(T_stdydsgn.stycitnumb,
                T_stdydsgn.stytype,
                T_stdydsgn.stynumgrp,
                0,
                T_stdydsgn.styserial)
            select count(*) into sg_cnt
            from subjgrp
            where sgcitnumb = T_stdydsgn.stycitnumb
            and sgdsgnnum = T_stdydsgn.styserial
            let T_stdydsgn.stynumgrp = sg_cnt
            display sg_cnt using "<<&",
                " Groups Entered" " at 19,40
                attribute(reverse)
            # needs flag to force jump to exposure groups
        else next field stynumgrp
        end if
    exit case
when x > T_stdydsgn.stynumgrp

```

```

    call alrt_box2()
    if upshift(answer) = "Y"
        then call find_sgrp(T_stdydsgn.stycitnumb,
            T_stdydsgn.styserial)
            select count(*) into sg_cnt
            from subjgrp
            where sgcitnumb = T_stdydsgn.stycitnumb
            and sgdsgnnum = T_stdydsgn.styserial
            let T_stdydsgn.stynumgrp = sg_cnt
            display sg_cnt using "<<&",
                "Groups Entered " at 19,40
                attribute(reverse)
            else next field stynumgrp
        end if
    exit case
end case
before field stynumexp
let numexpo = T_stdydsgn.stynumexp
select count(*) into x
from exporegm
where excitnumb = T_stdydsgn.stycitnumb
and exdsgnnum = T_stdydsgn.styserial
after field stynumexp
if T_stdydsgn.stynumexp > 99
    then
        error beep, "The maximum number of Exposure Regimens is 99!"
        next field stynumexp
    end if
case
    when x = T_stdydsgn.stynumexp
        next field stynumexp
    exit case
    when x < T_stdydsgn.stynumexp
        call add_details(T_stdydsgn.stycitnumb,
            T_stdydsgn.stytype,
            0,
            T_stdydsgn.stynumexp,
            T_stdydsgn.styserial)
        select count(*) into ex_cnt
        from exporegm
        where excitnumb = T_stdydsgn.stycitnumb
        and exdsgnnum = T_stdydsgn.styserial
        let T_stdydsgn.stynumexp = ex_cnt
        display ex_cnt using "<<&",
            "Regimens Entered " at 20,40
            attribute(reverse)
        # needs flag to force jump to exposure groups
    exit case
    when numexpo < T_stdydsgn.stynumexp
        call alrt_box1()
        if upshift(answer) = "Y"
            then
                call add_details(T_stdydsgn.stycitnumb,
                    T_stdydsgn.stytype,
                    0,
                    T_stdydsgn.stynumexp,
                    T_stdydsgn.styserial)

```

Toxin Knowledge System Source Code

```
        select count(*) into ex_cnt
        from exporegm
        where excitnumb = T_stdysgn.stycitnumb
        and exdsgnnum = T_stdysgn.styserial
        let T_stdysgn.stynumexp = ex_cnt
        display ex_cnt using "<<&",
        " Regimens Entered " at 20,40
        attribute(reverse)
        # needs flag to force jump to exposure groups
    else
        next field stynumexp
    end if
    exit case
when x > T_stdysgn.stynumexp
    call alrt_box2()
    if upshift(answer) = "Y"
    then
        call find_expo(T_stdysgn.stycitnumb,
            T_stdysgn.styserial)
        select count(*) into ex_cnt
        from exporegm
        where excitnumb = T_stdysgn.stycitnumb
        and exdsgnnum = T_stdysgn.styserial
        let T_stdysgn.stynumexp = ex_cnt
        display ex_cnt using "<<&",
        " Regimens Entered " at 20,40
        attribute(reverse)
    else
        next field stynumexp
    end if
    exit case
end case
end input
if dw = 1
    then return
    end if
update stdysgn
set stdysgn.* = T_stdysgn.*
    where styserial = tmp_styserial
(
    jump to exposure groups after change in number of subjects /
    exposures is needed here
)
message " Row updated. " attribute(reverse)
END FUNCTION
#####
FUNCTION delete_design(tmp_stycitnumb, tmp_styserial)
    define tmp_stycitnumb like stdysgn.stycitnumb,
        tmp_styserial integer,
        tmp_dsgn, tmp_totdsgn smallint
    call alrt265open()
    prompt "Do you want to delete this design overview? (y/n) > "
    for char answer
    IF upshift(answer) = "N"
    then
        MESSAGE "Row NOT deleted."
        sleep 1
```

```

MESSAGE ""
RETURN
else
  select excitnumb from exporegm
    where excitnumb = tmp_stycitnumb
    and exdsgnnum = tmp_styserial
  union
  select sgcitnumb from subjgrp
    where sgcitnumb = tmp_stycitnumb
    and sgdsngnum = tmp_styserial
  union
  select egcitnumb from expogrp
    where egcitnumb = tmp_stycitnumb
    and egdsng = tmp_styserial
  union
  select cfcitnumb from clinfind
    where cfcitnumb = tmp_stycitnumb
    and cfeglink = any
    (select egserial from expogrp
      where egdsng = tmp_styserial)
  if status = NOTFOUND
  then
    select count(*) into tmp_totdsgn
      from stdydsgn
      where stycitnumb = tmp_stycitnumb
    select stydsgncur into tmp_dsgn
      from stdydsgn
      where styserial = tmp_styserial
    DELETE FROM stdydsgn
      where styserial = tmp_styserial
    if tmp_dsgn < tmp_totdsgn then
      call renum_dsgn(tmp_stycitnumb, tmp_dsgn, tmp_totdsgn)
    end if
    select count(*) into tmp_totdsgn
      from stdydsgn
      where stycitnumb = tmp_stycitnumb
    update stdydsgn
      set stydsgntot = tmp_totdsgn
      where stycitnumb = tmp_stycitnumb
    update paperover
      set papnumdsgn = tmp_totdsgn
      where papcitnumb = tmp_stycitnumb
    MESSAGE "Row deleted."
    SLEEP 1
    MESSAGE ""
  else
    call blowdesign(tmp_stycitnumb, tmp_styserial)
  end if
end if
call alrt265close()
END FUNCTION
#####
FUNCTION blowdesign(tmp_stycitnumb, tmp_styserial)
define tmp_stycitnumb like stdydsgn.stycitnumb,
  tmp_styserial integer,
  tmp_totdsgn, tmp_dsgn, x smallint,
  hold_msg char(80)

```

Toxin Knowledge System Source Code

```
call alrt270open()
message beep, beep, beep,
"There are other tables linked to this record"
sleep 2
menu "DELETE DESIGN"
  COMMAND "Exit" HELP 2
  exit menu
  COMMAND "All-Links"
  "Delete all linked design-related tables. CAN BE DANGEROUS" HELP 514
  menu "Are you really sure you want to delete all these?"
  COMMAND "NO" HELP 515
  exit menu
  COMMAND "YES" HELP 516
  select unique(stydsngtot) into tmp_totdsgn
  from stydydsgn where stycitnumb = tmp_stycitnumb
  select stydsngcur into tmp_dsgn
  from stydydsgn
  where styserial = tmp_styserial
  DELETE FROM stydydsgn
  where styserial = tmp_styserial
  if tmp_dsgn < tmp_totdsgn then
    call renvum_dsgn(tmp_stycitnumb, tmp_dsgn, tmp_totdsgn)
  end if
  select count(*) into tmp_totdsgn
  from stydydsgn
  where stycitnumb = tmp_stycitnumb
  update stydydsgn
  set stydsngtot = tmp_totdsgn
  where stycitnumb = tmp_stycitnumb
  update paperover
  set papnumdsgn = tmp_totdsgn
  where papcitnumb = tmp_stycitnumb
  select count(*) into x from exporegm
  where excitnumb = tmp_stycitnumb
  and exdsgnnum = tmp_styserial
  display "" at 2,2
  call delete_expo(tmp_stycitnumb,tmp_styserial,0,0)
  display " ", x using "<<&", " exposure regimens deleted" at 2,2
  select count(*) into x from subjgrp
  where sgcitnumb = tmp_stycitnumb
  and sgdsgnnum = tmp_styserial
  display "" at 2,2
  call delete_sgrp(tmp_stycitnumb,tmp_styserial,0,0)
  display " ", x using "<<&", " subject groups deleted" at 2,2
  select count(*) into x from expogrp
  where egcitnumb = tmp_stycitnumb
  and egdsgn = tmp_styserial
  display "" at 2,2
  call delete_exgp(tmp_stycitnumb,tmp_styserial,0,0)
  display " ", x using "<<&", " exposure groups deleted" at 2,2
  exit menu
end menu
exit menu
end menu
call alrt270close()
END FUNCTION
```

#####

```
FUNCTION renum_dsgn(tmp_stycitnumb, del_dsgn, tot_dsgn)
```

```
  define
    tmp_stycitnumb like stdydsgn.stycitnumb,
    tmp_styserial integer,
    tmp_cur, del_dsgn, tot_dsgn smallint
  declare renum cursor for
    select styserial, stydsgncur
      into tmp_styserial, tmp_cur
    from stdydsgn
    where stycitnumb = tmp_stycitnumb
    and stydsgncur >= del_dsgn
    order by 2
  foreach renum
    update stdydsgn
      set stydsgncur = (stydsgncur - 1)
      where styserial = tmp_styserial
    call renum_exgp(tmp_stycitnumb, tmp_styserial, 0, 0)
  end foreach
END FUNCTION
```

```
#####
```

```
FUNCTION add_details(t_cit, t_type, t_subj, t_expo, t_dsgn)
```

```
{
  need to have a branch here for various designs
  for example, analytical design would need a different set of calls
}
```

```
define
  t_cit like stdydsgn.stycitnumb,
  t_type like stdydsgn.stytype,
  t_subj like stdydsgn.stynumgrp,
  t_expo like stdydsgn.stynumexp,
  t_dsgn integer,
  c_expo, c_subj smallint
case
  when t_subj = 0
    select count(*) into c_expo
    from exporegm
    where excitnumb = t_cit
    and exdsgnnum = t_dsgn
    if status = NOTFOUND
      then let c_expo = 0
    end if
    call add_expo(t_cit, c_expo, t_expo, t_dsgn)
  exit case
  when t_expo = 0
    select count(*) into c_subj
    from subjgrp
    where sgcitnumb = t_cit
    and sgdsgnnum = t_dsgn
    if status = NOTFOUND
      then let c_subj = 0
    end if
    call add_sgrp(t_cit, c_subj, t_subj, t_dsgn)
  exit case
otherwise
  call add_sgrp(t_cit, 0, t_subj, t_dsgn)
  call add_expo(t_cit, 0, t_expo, t_dsgn)
```


Toxin Knowledge System Source Code

```
        exit case
    end case
    current window is dsgnwin
END FUNCTION
#####
FUNCTION chk_cntl_chge()
    open window ck_cntl_chg at 10,10 with 2 rows, 50 columns
        attribute (border, reverse, prompt line first + 1)
    display " This will change existing data in the fields below. " at 1,1
        attribute (reverse)
    prompt " Continue? (y/N) " for answer
    close window ck_cntl_chg
    return answer
END FUNCTION
#####
FUNCTION alrt_box1()
    open window alrt_box1 at 10,10 with 2 rows, 50 columns
        attribute (border, reverse, prompt line first + 1)
    display " This value is greater than previously indicated. " at 1,1
        attribute (reverse)
    prompt " Do you want to add items? (y/n) > " for answer
    close window alrt_box1
END FUNCTION
#####
FUNCTION alrt_box2()
    open window alrt_box2 at 10,10 with 2 rows, 50 columns
        attribute (border, reverse, prompt line first + 1)
    display " This value is less than previously indicated. " at 1,1
        attribute (reverse)
    prompt " Do you want to remove items? (y/n) > " for answer
    close window alrt_box2
END FUNCTION
```

#tkssgrp.4gl

{TITLE: tkssgrp.4gl

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University of Illinois, CVM, IAPIC

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Contains the following functions:

```

    add_sgrp(tmp_sgcitnum, cursubj, tot_numsubj, tmp_design)
    find_sgrp(t_cit,t_dsgn)
    view_sgrp()
    disp_sgrp()
    update_sgrp(tmp_sgcitnum, tmp_sgserial)
    delete_sgrp(tmp_sgcitnum, sg_dsgn, sg_serial, del_flag)
    renum_subj(o_cit,n_cit,o_dsgn,o_subj,n_subj)

```

database tkstest

globals "tksglob.4gl"

#####

FUNCTION add_sgrp(tmp_sgcitnum, cursubj, tot_numsubj, tmp_design)

receiving (cit no., current subj no., total no. of subj, dsgn serial no.)

define

```

    tmp_design integer,
    tmp_sgcitnum, tmp_cit like subjgrp.sgcitnum),
    dsgnlabel smallint,
    totval, remain, let1, let2 smallint,
    tmp_link char(2),
    sextrans,ageunit char(20),
    tmp_sex, tmp_ar char(1),
    tmp_age, tmp_wr char(2),
    tmp_agerange char(10),
    imp_wtrange char(10),
    tot_numsubj, cursubj, x smallint

```

call swinopen()

clear form

let chosen = 1

display "" at 1,1

select stydsgncur into dsgnlabel

from stydsgn

where styserial = tmp_design

if status = NOTFOUND

then let dsgnlabel = tmp_design

end if

let sw = 0

for cnt = (cursubj+1) to tot_numsubj

INITIALIZE sgrp_array[cnt].* to null

end for

call set_count(tot_numsubj)

options help file "tkshelp.msg", help key control-w

input array sgrp_array from sgrp_rec.*

ON KEY (INTERUPT)

let sw = 1

exit input

ON Key(control-w)

case

when infield(sglink)

call showhelp(600)

Toxin Knowledge System Source Code

```

when infield(sgsource)
    call showhelp(602)
when infield(sgnunb)
    call showhelp(603)
when infield(sgsex)
    call showhelp(604)
when infield(sgage)
    call showhelp(605)
when infield(sgwt)
    call showhelp(606)
when infield(sght)
    call showhelp(607)
when infield(sgoccup)
    call showhelp(608)
when infield(sghlthstat)
    call showhelp(609)
when infield(sgtotexpo)
    call showhelp(610)
end case
BEFORE field sgcitnumb
    #initial displays
    display "" to sextrans
    display "" to ageunit
    display "" to agerange
    display "" to wtrange
    display by name tot_numsubj
    display by name dsnglabel
    curr_subj = arr_curr() + cursubj
    subj_cnt = arr_count() + cursubj
    let sgrp_array[curr_subj].sgserial = 0
    let sgrp_array[curr_subj].sglink = curr_subj
    display by name sgrp_array[curr_subj].sglink
    if tmp_sgcitnum is not null
        then
            let sgrp_array[curr_subj].sgcitnumb = tmp_sgcitnum
            let sgrp_array[curr_subj].sgdsgnnum = tmp_design
            display by name sgrp_array[curr_subj].sgcitnumb
            display by name sgrp_array[curr_subj].sgdsgnnum
        end if
    next field sgspecies
AFTER field sgcitnumb
    if sgrp_array[curr_arr].sgcitnumb is null
        then
            error "Must have Citation Number"
            next field sgcitnumb
        else
            let tmp_cit = sgrp_array[curr_arr].sgcitnumb
            let x = exist_citnumb(tmp_cit)
            if x = 0 then
                error "No CITATION DATA entered with this number."
                next field sgcitnumb
            end if
        end if
    before field sgsex
        call sex_choice()
    after field sgsex
        let tmp_sex = sgrp_array[curr_subj].sgsex

```

```

call sex_trans(tmp_sex) returning sextrans
if chosen = 0
  then next field sgsex
  else
    display by name sextrans
    call clear_choice(9,14,50)
  end if
before field sgageunit
call date_choice()
after field sgageunit
let tmp_age = sgrp_array[curr_subj].sgageunit
call date_trans(tmp_age) returning ageunit
if chosen = 0
  then next field sgageunit
  else
    display by name ageunit
    call clear_choice(9,14,50)
  end if
before field sgagerange
call agergrn_choice()
after field sgagerange
let tmp_ar = sgrp_array[curr_subj].sgagerange
call agergrn_tran(tmp_ar) returning tmp_agerange
if chosen = 0
  then
    next field sgagerange
  else
    display tmp_agerange to agerange
    call clear_choice(9,14,50)
  end if
before field sgwtunit
call wt_choice()
after field sgwtunit
case
  when sgrp_array[curr_subj].sgwtunit = "LB"
    let sgrp_array[curr_subj].sgwt = sgrp_array[curr_subj].sgwt / 2.2
    let sgrp_array[curr_subj].sgwtunit = "KG"
    display by name sgrp_array[curr_subj].sgwt
    display by name sgrp_array[curr_subj].sgwtunit
    exit case
  when sgrp_array[curr_subj].sgwtunit = "OZ"
    let sgrp_array[curr_subj].sgwt = sgrp_array[curr_subj].sgwt / 16 / 2.2
    let sgrp_array[curr_subj].sgwtunit = "KG"
    display by name sgrp_array[curr_subj].sgwt
    display by name sgrp_array[curr_subj].sgwtunit
    exit case
  when sgrp_array[curr_subj].sgwtunit = "GM"
    let sgrp_array[curr_subj].sgwt = sgrp_array[curr_subj].sgwt / 1000
    let sgrp_array[curr_subj].sgwtunit = "KG"
    display by name sgrp_array[curr_subj].sgwt
    display by name sgrp_array[curr_subj].sgwtunit
    exit case
  when sgrp_array[curr_subj].sgwtunit = "KG"
    let sgrp_array[curr_subj].sgwt = sgrp_array[curr_subj].sgwt
    let sgrp_array[curr_subj].sgwtunit = "KG"
    display by name sgrp_array[curr_subj].sgwt
    display by name sgrp_array[curr_subj].sgwtunit

```

Toxin Knowledge System Source Code

```
        exit case
    otherwise
        error "Indicated units are not acceptable!"
        sleep 1
        next field sgwtunit
    exit case
end case
call clear_choice(9,14,50)
before field sgwtrange
    call wrangeChoice() returning sgrp_array[curr_subj].sgwtrange
after field sgwtrange
    let tmp_wr = sgrp_array[curr_subj].sgwtrange
    call wtrgn_tran(tmp_wr) returning tmp_wtrange
    if chosen = 0
        then
            next field sgwtrange
        else
            display tmp_wtrange to wtrange
            call clear_choice(9,14,50)
        end if
    after field sgtotexpo
        if subj_cnt = tot_numsubj
            then exit input
        end if
    end input
if sw = 1 then return end if
for cnt = (cursubj+1) to subj_cnt
    insert into subjgrp values(sgrp_array[cnt].*)
end for
call swinclose()
END FUNCTION
#####
FUNCTION flnd_sgrp(t_cit,t_dsgn) (citation, design serial number)
define
    t_cit like subjgrp.sgcitnumb,
    t_dsgn integer
call swinopen()
case
    when (t_cit is null and t_dsgn = 0)
        clear form
        message "Enter search criteria and hit ESC to search"
        let int_flag = 0
        construct by name query1 on subjgrp.*
        if int_flag <> 0 then return end if
        let select1 = "select * from subjgrp where ",
            query1 clipped,
            " order by sgcitnumb, sgdsgnnum, sglink"
        let select2 = "select count(*) from subjgrp where ",
            query1 clipped
        exit case
    when (t_cit is not null and t_dsgn = 0)
        let select1 = "select * from subjgrp where sgcitnumb = ",
            quote, t_cit clipped, quote,
            " order by sgcitnumb, sgdsgnnum, sglink"
        let select2 = "select count(*) from subjgrp where sgcitnumb = ",
            quote, t_cit clipped, quote
        exit case
```

```

otherwise
    let select1 = "select * from subjgrp where ",
        "sgcitnumb = ", quote, t_cit clipped, quote,
        " and sgdsgrnum = ", t_dsgn,
        " order by sgcitnumb, sgdsgrnum, sglink"
    let select2 = "select count(*) from subjgrp where ",
        "sgcitnumb = ", quote, t_cit clipped, quote,
        " and sgdsgrnum = ", t_dsgn
    exit case
end case
prepare cnt_subjgrp from select2
prepare slct_subjgrp from select1
display "Searching . . . " at 21,2 attribute(reverse)
declare cnt_curs cursor for cnt_subjgrp
    foreach cnt_curs into cnt
        end foreach
declare s_curs scroll cursor for slct_subjgrp
open s_curs
call view_sgrp()
close s_curs
end function
#####
FUNCTION view_sgrp()
    FETCH FIRST s_curs into T_subjgrp.*
    if status = NOTFOUND
        THEN
            MESSAGE "No subjects found."
            SLEEP 1
            MESSAGE ""
        else
            let tmp_cnt = 1
            call disp_sgrp()
            display "" at 21,2
            display " ", tmp_cnt, " of ", cnt, " rows found." at 21,2
        end if
    MENU "BROWSE"
        COMMAND "Next"
            "View the next Subject Group in the list." HELP 170
            FETCH NEXT s_curs into T_subjgrp.*
            let tmp_cnt = tmp_cnt + 1
            if status = NOTFOUND THEN
                message "No more Subject Groups in this direction."
                sleep 1
                let tmp_cnt = cnt
                message ""
                fetch last s_curs into T_subjgrp.*
            end if
            display "" at 21,2
            display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
            attribute(reverse)
            call disp_sgrp()
        COMMAND "Previous"
            "View the previous Subject Groups in the list." HELP 170
            FETCH PREVIOUS s_curs into T_subjgrp.*
            let tmp_cnt = tmp_cnt - 1
            if status = NOTFOUND THEN
                message "No more Subject Groups in this direction."

```

Toxin Knowledge System Source Code

```
        sleep 1
        message ""
        let tmp_cnt = 1
        fetch first s_curs into T_subjgrp.*
        end if
        display "" at 21,2
        display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
        attribute(reverse)
        call disp_sgrp()
    COMMAND "First"
        "View the first Subject Group in the list." HELP 170
        FETCH FIRST s_curs into T_subjgrp.*
        let tmp_cnt = 1
        display "" at 21,2
        display " ", tmp_cnt, " of ", cnt, " rows" at 21,2
        attribute(reverse)
        call disp_sgrp()
    COMMAND "Last"
        "View the last Subject Group in the list." HELP 170
        message "Searching for last record...."
        FETCH LAST s_curs into T_subjgrp.*
        let tmp_cnt = cnt
        message ""
        display "" at 21,2
        display " ", tmp_cnt, " of ", cnt, " row" at 21,2
        attribute(reverse)
        call disp_sgrp()
    COMMAND "Update"
        "Update Subject data" HELP 171
        call update_sgrp(T_subjgrp.sgcitnumb,T_subjgrp.sgserial)
        call disp_sgrp()
    COMMAND "Delete"
        "Delete this entry from the database<submenu>" HELP 611
        call delete_sgrp(T_subjgrp.sgcitnumb, T_subjgrp.sgdsgnum,T_subjgrp.sgserial,1)
        call disp_sgrp()
    COMMAND "Query-Again"
        "Enter new search criteria" HELP 612
        close s_curs
        let citnumber = ""
        let hold_dsgn = 0
        call find_sgrp(citnumber,hold_dsgn)
        exit menu
    COMMAND "Exit"
        "Leave this menu." HELP 2
        close _curs
        exit menu
    end menu
    close s_curs
END FUNCTION

#####
FUNCTION disp_sgrp()
    define
        tot_numsubj smallint,
        dsgnlabel integer,
        agerange, wtrange char(20),
        sextrans,ageunit char(20)
    select count(*) into tot_numsubj
```

```

    from subjgrp
    where sgcitnumb = T_subjgrp.sgcitnumb
    and sgdsgnnum = T_subjgrp.sgdsgnnum
display by name T_subjgrp.*
call sex_trans(T_subjgrp.sgsex) returning sextrans
display by name sextrans
call date_trans(T_subjgrp.sgageunit) returning ageunit
display by name ageunit
call agerng_tran(T_subjgrp.sgagerange) returning agerange
    display by name agerange
call wtrng_tran(T_subjgrp.sgwtrange) returning wtrange
    display by name wtrange
display by name tot_numsubj
select stydsgncur into dsgnlabel
    from stydsgn
    where styserial = T_subjgrp.sgdsgnnum
display by name dsgnlabel
END FUNCTION
#####
FUNCTION update_sgrp(tmp_sgcitnum, tmp_sgserial)
define
    tmp_sgserial integer,
    tmp_sgcitnum like subjgrp.sgcitnumb,
    sextrans,ageunit char(20),
    tmp_sex, tmp_ar char(1),
    tmp_age, tmp_wr char(2),
    tmp_agrange char(10),
    tmp_wtrange char(10),
    tmp_dsgn like subjgrp.sgdsgnnum,
    list_flag, tmp_sgnum, sg_cnt smallint
let sw = 0
display tmp_sgcitnum to sgcitnumb
display tmp_sgserial to sgserial
INPUT T_subjgrp.* without defaults from sg.p_rec.*
    ON KEY (INTERRUPT)
        let sw = 1
        exit input
before field sgcitnumb
    select stydsgncur into tmp_dsgn
        from stydsgn
        where styserial = T_subjgrp.sgdsgnnum
    display tmp_dsgn to dsgnlabel
    select count(*) into sg_cnt
        from subjgrp
        where sgdsgnnum = T_subjgrp.sgdsgnnum
    display sg_cnt to tot_numsubj
after field sgcitnumb
    message "Hit ESCAPE to update row"
    if T_subjgrp.sgcitnumb is null
        then
            error "Must have citnumber!"
        end if
    if tmp_sgcitnum <> T_subjgrp.sgcitnumb then
        call exist_citnumb(T_subjgrp.sgcitnumb) returning x
        if x = 0
            then
                error beep, "No CITATION entered with this NUMBER "

```


Toxin Knowledge System Source Code

```

        next field sgcitnumb
    else
        select count(*) into x
        from subjgrp
        where sgcitnumb = T_subjgrp.sgcitnumb
        if x > 0 then
            error "SUBJECT data already entered for this paper."
            sleep 2
            next field sgcitnumb
        end if
    end if
end if
after field sgdsgrnum
    select stydsgrncur into tmp_dsgn
    from stydsgrn
    where styserial = T_subjgrp.sgdsgrnum
    display tmp_dsgn to dsgnlabel
before field sgsex
    call sex_choice()
after field sgsex
    call sex_trans(T_subjgrp.sgsex) returning sextrans
    if chosen = 0
        then next field sgsex
    else
        display by name sextrans
        call clear_choice(9,14,50)
    end if
before field sgageunit
    call date_choice()
after field sgageunit
    call date_trans(T_subjgrp.sgageunit) returning ageunit
    if chosen = 0
        then next field sgageunit
    else
        display by name ageunit
        call clear_choice(9,14,50)
    end if
before field sgagerange
    call agergrn_choice()
after field sgagerange
    let tmp_ar = T_subjgrp.sgagerange
    call agergrn_tran(tmp_ar) returning tmp_agerange
    if chosen = 0
        then
            next field sgagerange
        else
            display tmp_agerange to agerange
            call clear_choice(9,14,50)
        end if
before field sgwtunit
    call wt_choice()
after field sgwtunit
    case
        when T_subjgrp.sgwtunit = "LB"
            let T_subjgrp.sgrwt = T_subjgrp.sgwt * 2.2
            let T_subjgrp.sgwtunit = "KG"
            display by name T_subjgrp.sgrwt

```

```

        display by name T_subjgrp.sgwtunit
        exit case
    when T_subjgrp.sgwtunit = "OZ"
        let T_subjgrp.sgwt = T_subjgrp.sgwt / 16 * 2.2
        let T_subjgrp.sgwtunit = "KG"
        display by name T_subjgrp.sgwt
        display by name T_subjgrp.sgwtunit
        exit case
    when T_subjgrp.sgwtunit = "GM"
        let T_subjgrp.sgwt = T_subjgrp.sgwt / 1000
        let T_subjgrp.sgwtunit = "KG"
        display by name T_subjgrp.sgwt
        display by name T_subjgrp.sgwtunit
        exit case
    when T_subjgrp.sgwtunit = "KG"
        let T_subjgrp.sgwt = T_subjgrp.sgwt
        let T_subjgrp.sgwtunit = "KG"
        display by name T_subjgrp.sgwt
        display by name T_subjgrp.sgwtunit
        exit case
    otherwise
        error "Indicated units are not acceptable!"
        sleep 1
        next field sgwtunit
        exit case
    end case
    call clear_choice(9,14,50)
    before field sgwtrange
        call wrangeChoice() returning T_subjgrp.sgwtrange
    after field sgwtrange
        let tmp_wr = T_subjgrp.sgwtrange
        call wrngn_tran(tmp_wr) returning tmp_wtrange
        if chosen = 0
            then
                next field sgwtrange
            else
                display tmp_wtrange to wtrange
                call clear_choice(9,14,50)
            end if
        end if

    End Input
    if sw = 1 then return end if
    UPDATE subjgrp set subjgrp.* = T_subjgrp.*
    where subjgrp.sgserial = tmp_sgserial
    END FUNCTION
#####
FUNCTION delete_sgrp(tmp_sgcltnum, sg_dsgn, sg_serial, del_flag)
    define tmp_sgcltnum like subjgrp.sgcltnumb,
        sg_dsgn like subjgrp.sgdsgnnum,
        sg_serial integer,
        del_flag, tot_sg, sg_lnk smallint
    if del_flag <> 0
        then
            call alrt260open()
            PROMPT "Do you want to delete this Subject Group? (y/n) "
            for char answer
            If upshift(answer) = "N"

```

Toxin Knowledge System Source Code

```

    then
        message "Row NOT deleted"
        sleep 1
        Message ""
        call alrt260close()
        return
    else
        if sg_serial = 0
            then
                DELETE FROM subjgrp
                where sgcitnumb = tmp_sgcitnum
                and sgdsgnnum = sg_dsgn
                clear form
            else
                select count(*) into tot_sg
                from subjgrp
                where sgcitnumb = tmp_sgcitnum
                and sgdsgnnum = sg_dsgn
                select sglink into sg_lnk
                from subjgrp
                where sgserial = sg_serial
                DELETE FROM subjgrp
                where sgserial = sg_serial
                if sg_lnk < tot_sg then
                    for x = sg_lnk to tot_sg
                        call renum_subj(tmp_sgcitnum,"0", sg_dsgn, x+1, x)
                    end for
                end if
                if del_flag <> 0
                    then
                        Message "ROW DELETED."
                        sleep 1
                        Message ""
                        call alrt260close()
                    end if
                end if
            end if
        end if
    end FUNCTION
#####
FUNCTION renum_subj(o_cit,n_cit,o_dsgn,o_subj,n_subj)
# This probably needs an internal loop to manage the counting
define
    o_cit,n_cit like subjgrp.sgcitnumb,
    o_dsgn integer,
    o_subj, n_subj like subjgrp.sglink
update subjgrp
set sglink = n_subj
where sgcitnumb = o_cit
and sglink = o_subj
and sgdsgnnum = o_dsgn
call renum_exgp(o_cit,n_cit,o_dsgn,o_subj,n_subj,0,0)
end FUNCTION

```

#tksexpo.4gl

{Title: tksexpo.4gl

Copyright Harold L. Trammel, 1987-1988

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Contains the following functions:

```

add_expo(ex_cit, tmp_numexpo, tot_numexpo, tmp_design)
find_expo(t_cit,t_dsgn)
view_expo()
disp_expo()
update_expo(tmp_citno,tmp_serial)
delete_expo(ex_cit, ex_dsgn, ex_serial, del_flag)
renum_expo(o_cit,n_cit,o_dsgn,n_dsgn,o_expo,n_expo)

```

database tkstest

globals "tksglob.4gl"

#####

FUNCTION add_expo(ex_cit, tmp_numexpo, tot_numexpo, tmp_design)

citation num, current expo cnt, tot num of expo, design serial num

define

```

formulation, route, purpose char(10),
ex_cit like exporegm.excitnumb,
tmp_design integer,
tmp_2ch char(2),
tmp_3ch char(3),
dsgnlabel,tmp_numexpo, tot_numexpo smallint,
ew, curr_exp, exp_cnt, xsmallint

```

#initial setup

```

call expwinopen()
display "" at 1,1
clear form
let ew = 0
select stydsgncur into dsgnlabel
from stydsgn
where styserial = tmp_design
if status = NOTFOUND
then let dsgnlabel = tmp_design
end if
for cnt = (tmp_numexpo+1) to tot_numexpo
initialize expo_array[cnt].* to null
end for
call set_count(tot_numexpo)
options help file "tkshelp.msg",
help key CONTROL-w
input array expo_array from exp_rec.*
on key(interrupt)
let ew = 1
exit input
On Key(control-w)
case
when infield(expurpose)
call showhelp(701)
when infield(exagent)
call showhelp(702)
when infield(exdose)
call showhelp(703)

```

Toxin Knowledge System Source Code

```
        when infield(exformul)
            call showhelp(704)
        when infield(exroute)
            call showhelp(705)
        when infield(exinterval)
            call showhelp(706)
        when infield(exduration)
            call showhelp(707)
        when infield(exadminmeth)
            call showhelp(708)
        when infield(exevaltime)
            call showhelp(709)
        end case

before field excitnumb
    let curr_exp = arr_curr() + tmp_numexpo
    let exp_cnt = arr_count() + tmp_numexpo
    let expo_array[curr_exp].exdsgnnum = tmp_design
    let expo_array[curr_exp].exserial = 0
    let expo_array[curr_exp].exlink = curr_exp
    #initial displays
        display "" to frm_only.formulation
        display "" to frm_only.route
        display "" to frm_only.purpose
        display ex_cit to excitnumb
        display by name tot_numexpo
        display by name dsgnlabel
        display by name expo_array[curr_exp].exdsgnnum
        display by name expo_array[curr_exp].exlink
    if ex_cit is not null
        then
            let expo_array[curr_exp].excitnumb = ex_cit
            display by name expo_array[curr_exp].excitnumb
            next field expurpose
        end if
before field expurpose
    call pur_choice()
after field expurpose
    let tmp_3ch = expo_array[curr_exp].expurpose
    call pur_trans(tmp_3ch) returning purpose
    if chosen = 0
        then next field expurpose
        else display by name purpose
    end if
    call clear_choice(9,14,52)
before field exdoseunit
    call dose_choice()
before field exformul
    call form_choice()
after field exformul
    let tmp_2ch = expo_array[curr_exp].exformul
    call form_trans(tmp_2ch) returning formulation
    if chosen = 0
        then next field exformul
        else display by name formulation
    end if
before field exroute
```

```

        call rte_choice()
    after field exroute
        let tmp_2ch = expo_array[curr_exp].exroute
        call rte_trans(tmp_2ch) returning route
        if chosen = 0
            then next field exroute
            else display by name route
            end if
        call clear_choice(9,18,52)
    after field exevaltime
        if exp_cnt = tot_numexpo
            then exit input
            end if
    end input
options help key control-w
if ew = 1
    then return
    end if
for cnt = (tmp_numexpo + 1) to exp_cnt
    insert into exporegm values (expo_array[cnt].*)
end for
call expwinclose()
end FUNCTION
#####
FUNCTION flnd_expo(t_cit,t_dsgn) {citation, design serial number}
define
    t_cit like exporegm.excitnumb,
    t_dsgn integer
call expwinopen()
case
    when (t_cit is null and t_dsgn = 0)
        clear form
        message "Enter search criteria and hit ESC to search"
        let int_flag = 0
        construct by name query1 on exporegm.*
        if int_flag <> 0 then return end if
        let select1 = "select * from exporegm where ",
            query1 clipped;
            "order by excitnumb, exdsgnnum, exlink"
        let select2 = "select count(*) from exporegm where ",
            query1 clipped
        exit case
    when (t_cit is not null and t_dsgn = 0)
        let select1 = "select * from exporegm where excitnumb = ",
            quote, t_cit clipped, quote,
            "order by excitnumb, exdsgnnum, exlink"
        let select2 = "select count(*) from exporegm where excitnumb = ",
            quote, t_cit clipped, quote
        exit case
    otherwise
        let select1 = "select * from exporegm where ",
            "excitnumb = ",quote, t_cit clipped,quote,
            "and exdsgnnum = ", t_dsgn,
            "order by excitnumb, exdsgnnum, exlink"
        let select2 = "select count(*) from exporegm where ",
            "excitnumb = ",quote, t_cit clipped,quote,
            "and exdsgnnum = ", t_dsgn

```

Toxin Knowledge System Source Code

```
        exit case
    end case
    prepare cnt_expo from select2
    prepare select_expo from select1
    display "Searching . . . " at 20,2 attribute(reverse)
    declare cnt_curs cursor for cnt_expo
        foreach cnt_curs into cnt
            end foreach
    declare e_curs scroll cursor for select_expo
    open e_curs
    call view_expo()
end FUNCTION

#####
FUNCTION view_expo()
    fetch first e_curs into T_exporegm.*
    if status = NOTFOUND
        then
            MESSAGE "No exposures found."
            SLEEP 1
            MESSAGE ""
        else
            let tmp_cnt = 1
            call disp_expo()
            display "" at 20,2
            display " ", tmp_cnt, " of ", cnt, " rows found." at 20,2
        end if
    MENU "BROWSE"
    COMMAND "Next"
        "View the next Exposure Regimen in the list." HELP 170
        FETCH NEXT e_curs INTO T_exporegm.*
        let tmp_cnt = tmp_cnt + 1
        IF status = NOTFOUND THEN
            MESSAGE "No more Exposure Regimens in this direction."
            SLEEP 1
            let tmp_cnt = cnt
            MESSAGE ""
            FETCH LAST e_curs INTO T_exporegm.*
            END IF
        display "" at 20,2
        display " ", tmp_cnt, " of ", cnt, " rows" at 20,2
        attribute(reverse)
        call disp_expo()
    COMMAND "Previous"
        "View the Previous Exposure Regimen in the list." HELP 170
        FETCH PREVIOUS e_curs INTO T_exporegm.*
        let tmp_cnt = tmp_cnt - 1
        IF status = NOTFOUND THEN
            MESSAGE "No more Exposure Regimens in this direction."
            SLEEP 1
            MESSAGE ""
            let tmp_cnt = 1
            FETCH FIRST e_curs INTO T_exporegm.*
            END IF
        display "" at 20,2
        display " ", tmp_cnt, " of ", cnt, " rows" at 20,2
        attribute(reverse)
        call disp_expo()
```

```

COMMAND "First"
  "View the first Exposure Regimen in the list." HELP 170
  FETCH FIRST e_curs INTO T_exporegm.*
  let tmp_cnt = 1
  display "" at 20,2
  display " ",tmp_cnt, " of ", cnt, " rows" at 20,2
  attribute(reverse)
  call disp_expo()
COMMAND "Last"
  "View the Last Exposure Regimen in the list." HELP 170
  message "Searching for last record...."
  FETCH LAST e_curs INTO T_exporegm.*
  let tmp_cnt = cnt
  message ""
  display "" at 20,2
  display " ",tmp_cnt, " of ", cnt, " rows" at 20,2
  attribute(reverse)
  call disp_expo()
command "Update"
  "Update Exposure Data" HELP 171
  call update_expo(T_exporegm.excitnumb,T_exporegm.exserial)
  call disp_expo()
command "Delete"
  "Delete this entry from database <submenu>" HELP 715
  call delete_expo(T_exporegm.excitnumb,0,T_exporegm.exlink,1)
  call disp_expo()
COMMAND "Query-again"
  "Enter new search criteria" HELP 716
  close e_curs
  let citnumber = ""
  call find_expo(citnumber,0)
  exit menu
COMMAND "Exit"
  "Leave this menu" HELP 2
  close e_curs
  EXIT MENU
END MENU
end FUNCTION
#####
FUNCTION disp_expo()
  define
    tmp_formul char(10),
    formulation, route, purpose char(10),
    tmp_route char(10),
    tmp_numexp char(2),
    dsgnlabel integer
  select unique(stynumexp) into tmp_numexp
  from stdydsgn
  where styserial = T_exporegm.exdsgnnum
  select stydsgncur into dsgnlabel
  from stdydsgn
  where styserial = T_exporegm.exdsgnnum
  display by name dsgnlabel
  display by name T_exporegm.*
  display tmp_numexp to tot_numexpo
  call pur_trans(T_exporegm.expurpose) returning purpose
  display by name purpose

```


Toxin Knowledge System Source Code

```
call form_trans(T_exporegm.exformul) returning formulation
display by name formulation
call rte_trans(T_exporegm.exroute) returning route
display by name route
end FUNCTION
#####
FUNCTION update_expo(tmp_citno,tmp_serial)
define
    formulation, route, purpose char(10),
    tmp_citno like exporegm.excitnumb,
    tmp_exno like exporegm.exlink,
    tmp_dsgn like exporegm.exdsgnnum,
    tmp_serial integer,
    x, ew, curr_exp, exp_cnt smallint
let ew = 0
display tmp_citno to excitnumb
display tmp_serial to exserial
input by name T_exporegm.* without defaults
on key(interrupt)
    let ew = 1
    exit input
before field excitnumb
    select stydsgncur
        into tmp_dsgn
        from stdydsgn
        where styserial = T_exporegm.exdsgnnum
    display tmp_dsgn to dsgnlabel
    select count(*)
        into exp_cnt
        from exporegm
        where exdsgnnum = T_exporegm.exdsgnnum
    display exp_cnt to tot_numexpo
after field exdsgnnum
    select stydsgncur
        into tmp_dsgn
        from stdydsgn
        where styserial = T_exporegm.exdsgnnum
    display tmp_dsgn to dsgnlabel
    select count(*)
        into exp_cnt
        from exporegm
        where exdsgnnum = T_exporegm.exdsgnnum
    display exp_cnt to tot_numexpo
before field expurpose
    call pur_choice()
after field expurpose
    call pur_trans(T_exporegm.expurpose) returning purpose
    if chosen = 0
        then next field expurpose
        else display by name purpose
    end if
    call clear_choice(9,18,52)
before field exdoseunit
    call dose_choice()
before field exformul
    call form_choice()
after field exformul
```

```

    call form_trans(T_exporegm.exformul) returning formulation
    if chosen = 0
        then next field exformul
        else display by name formulation
        end if
    before field exroute
        call rte_choice()
    after field exroute
        call rte_trans(T_exporegm.exroute) returning route
        if chosen = 0
            then next field exroute
            else display by name route
            end if
        call clear_choice(9,18,52)
    end input
    if ew = 1
        then return
        end if
    update exporegm set exporegm.* = T_exporegm.*
        where exporegm.exserial = tmp_serial
    # Logic question
    (
        question the logic of this part
        if (T_exporegm.excitnumb <> tmp_citno or
            T_exporegm.exdsgnnum <> tmp_dsgn or
            T_exporegm.exlink <> tmp_exno)
            then
                call renum_expo(tmp_citno, T_exporegm.excitnumb,
                    tmp_dsgn, T_exporegm.exdsgnnum,
                    tmp_exno, T_exporegm.exlink)
            link to the expogrp tables maintained in renum_expo
            end if
        )

    end FUNCTION
#####
FUNCTION delete_expo(ex_cit, ex_dsgn, ex_serial, del_flag)
    # ex_dsgn = 0 to delete only this lnk
    # ex_serial = 0 to delete all of dsgn(x)
    # del_flag to control dialog box

    define ex_cit like exporegm.excitnumb,
        ex_dsgn like exporegm.exdsgnnum,
        ex_serial like exporegm.exlink,
        ex_lnk, del_flag, tot_ex smallint
    if del_flag <> 0
        then
            call alrt260open()
            PROMPT "Do you want to delete this Exposure Regimen? (y/n) "
            for answer
                If upshift(answer) = "N"
                    then
                        message "Row NOT deleted"
                        sleep 1
                        Message ""
                        call alrt260close()
                        return

```

Toxin Knowledge System Source Code

```
else
  if ex_serial = 0
    then
      DELETE FROM exporegm
        where excitnumb = ex_cit
        and exdsgnnum = ex_dsgn
    else
      select count(*) into tot_ex
        from exporegm
        where excitnumb = ex_cit
        and exdsgnnum = ex_dsgn
      select exlink into ex_lnk
        from exporegm
        where exserial = ex_serial
      DELETE FROM exporegm
        where exserial = ex_serial
      if ex_lnk < tot_ex then
        for x = ex_lnk to tot_ex
          call renum_expo(ex_cit,"0",ex_dsgn,"0",x+1,x)
        end for
      end if
      if del_flag <> 0
        then
          Message "ROW DELETED."
          sleep 1
          Message ""
          call alrt260close()
        end if
      end if
    end if
  end if
end FUNCTION
#####
FUNCTION renum_expo(o_cit,n_cit,o_dsgn,n_dsgn,o_expo,n_expo)
  define o_cit,n_cit like exporegm.excitnumb,
    o_dsgn,n_dsgn like exporegm.exdsgnnum,
    o_expo,n_expo like exporegm.exlink
  if n_dsgn > 0
    then
      update exporegm
        set exdsgnnum = n_dsgn
        where excitnumb = o_cit
        and exdsgnnum = o_dsgn
    else
      update exporegm
        set exlink = n_expo
        where excitnumb = o_cit
        and exlink = o_expo
        and exdsgnnum = o_dsgn
    end if
  {
    need some mechanism to renumber exposure group data
  }
end FUNCTION
```

#tksexpgrp.4gl

(Comments:

Title: tksexpgrp.4gl

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University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Purpose: to establish links between regimens and groups

Contains the following functions:

add_exgp(t_citnumber)

find_exgp(t_cit)

view_exgp()

disp_exgp()

update_exgp(tmp_citnumb, tmp_egserial)

delete_exgp(tmp_citnumb, tmp_dsgn, tmp_egserial, del_flag)

renum_exgp(t_cit, t_dsgn, t_sg, t_ex)

)

database tkstest

globals "tksglob.4gl"

#####

FUNCTION add_exgp(t_citnumber)

define

hold_serial integer,

hold_descript like expogrp.egdsgndsc,

t_citnumber like expogrp.egcitnumb,

tmp_dsgnlbl like expogrp.egdsgnlabel,

tmp_dsgn like expogrp.egdsgn,

tmp_subj, tmp_expo smallint,

numexgp smallint,

pge integer,

p_numdsgn, eg, x, y, curr_exgp, exgp_cnt smallint

#initial setup

call linkwinopen()

clear form

display "" at 1,1

let eg=0

for cnt = 1 to 50

initialize exgp_array[cnt].* to null

end for

call set_count(50)

options help file "tkshelp.msg",

help key CONTROL-w

if t_citnumber is null

then prompt "Which citation? " for t_citnumber

let t_citnumber = upshift(t_citnumber)

select count(*) into cnt from citation

where citnumb = t_citnumber

if cnt < 1 then

ERROR "Must add citation with this number > ",

t_citnumber

end if

end if

input array exgp_array from exgp_rec.*

on key(interrupt)

let eg=1

exit input

Toxin Knowledge System Source Code

```
on key(CONTROL-w)
  case
    # these need to be updated 3/21/89
    when infield(egcitnumb)
      call showhelp(800)
    when infield(egdsgndsc)
      call showhelp(801)
    when infield(egsubgdsc)
      call showhelp(802)
    when infield(egexpodsc)
      call showhelp(803)
    when infield(egtotnum)
      call showhelp(804)
    end case

before field egcitnumb
  let curr_exgp = arr_curr()
  let exgp_cnt = arr_count()
  let exgp_array[curr_exgp].egserial = 0
  if t_citnumber is not null
    then
      let exgp_array[curr_exgp].egcitnumb = t_citnumber
      display by name exgp_array[curr_exgp].egcitnumb
      select count(*) into numexgp
        from expogrp
        where egcitnumb = t_citnumber
      let y = curr_exgp + numexgp
      let exgp_array[curr_exgp].egtotnum = exgp_cnt+numexgp
      display y to eignum
      display by name exgp_array[curr_exgp].egtotnum
      next field egdsgnlabel
    end if
before field egdsgnlabel
  call show_dsgn(t_citnumber, 0) returning pge
  message "Use CNTL-P to show Previous page, CNTL-N to show Next page "
  on key (CONTROL-P)
    if infield(egdsgnlabel)
      then
        call show_dsgn(t_citnumber, pge-1) returning pge
      end if
  on key (CONTROL-N)
    if infield(egdsgnlabel)
      then
        call show_dsgn(t_citnumber, pge+1) returning pge
      end if
after field egdsgnlabel
  let tmp_dsgnlbl = exgp_array[curr_exgp].egdsgnlabel
  call gen_dsgdsc(t_citnumber, tmp_dsgnlbl)
    returning hold_descript, hold_serial
  let exgp_array[curr_exgp].egdsgndsc = hold_descript
  let exgp_array[curr_exgp].egdsgn = hold_serial
  display by name exgp_array[curr_exgp].egdsgndsc
  display by name exgp_array[curr_exgp].egdsgn
before field egsubglabel
  let tmp_dsgn = exgp_array[curr_exgp].egdsgn
  call show_subj(t_citnumber, tmp_dsgn, 0) returning pge
  message "Use CNTL-P to show Previous page, CNTL-N to show Next page "
```

```

on key (CONTROL-P)
  call show_subj(t_citnumber, tmp_dsgn, pge-1) returning pge
on key (CONTROL-N)
  call show_subj(t_citnumber, tmp_dsgn, pge+1) returning pge
after field egsublabel
  let tmp_subj = exgp_array[curr_exgp].egsublabel
  call gen_subdsc(t_citnumber, tmp_dsgn, tmp_subj)
  returning hold_descript, hold_serial
  let exgp_array[curr_exgp].egsubgdsc = hold_descript
  let exgp_array[curr_exgp].egsubg = hold_serial
  display by name exgp_array[curr_exgp].egsubgdsc
  display by name exgp_array[curr_exgp].egsubg
before field egexpolabel
  call show_expo(t_citnumber, tmp_dsgn, 0) returning pge
  message "Use CNTL-P to show Previous page, CNTL-N to show Next page "
on key (CONTROL-P)
  if infield(egexpolabel) then
    call show_expo(t_citnumber, tmp_dsgn, pge-1) returning pge
  end if
on key (CONTROL-N)
  if infield(egexpolabel) then
    call show_expo(t_citnumber, exgp_array[curr_exgp].egdsgn, pge+1) returning pge
  end if
after field egexpolabel
  let tmp_expo = exgp_array[curr_exgp].egexpolabel
  call gen_expdsc(t_citnumber, tmp_dsgn, tmp_expo)
  returning hold_descript, hold_serial
  let exgp_array[curr_exgp].egexpodsc = hold_descript
  let exgp_array[curr_exgp].egexpo = hold_serial
  display by name exgp_array[curr_exgp].egexpodsc
  display by name exgp_array[curr_exgp].egexpo
  let exgp_array[curr_exgp].eglink = "D",
    exgp_array[curr_exgp].egdsgnlabel using "<<", "S",
    exgp_array[curr_exgp].egsublabel using "<<", "E",
    exgp_array[curr_exgp].egexpolabel using "<<"
  display by name exgp_array[curr_exgp].eglink
end input
options help key CONTROL-w
if eg = 1
  then return
end if
for cnt = 1 to exgp_cnt
  insert into expogrp values
    (exgp_array[cnt].egcitnumb,
     exgp_array[cnt].egserial,
     exgp_cnt,
     exgp_array[cnt].eglink,
     exgp_array[cnt].egdsgn,
     exgp_array[cnt].egdsgnlabel,
     exgp_array[cnt].egdsgndsc,
     exgp_array[cnt].egsubg,
     exgp_array[cnt].egsublabel,
     exgp_array[cnt].egsubgdsc,
     exgp_array[cnt].egexpo,
     exgp_array[cnt].egexpolabel,
     exgp_array[cnt].egexpodsc)
end for

```

Toxin Knowledge System Source Code

```
select count(*) into y from expogrp
  where egcnumb = t_citnumber
update expogrp
  set egtotnum = y
  where egcnumb = t_citnumber
END FUNCTION
#####
FUNCTION flnd_exgp(t_cit)
  define
    t_cit like expogrp.egcnumb
  call linkwinopen()
  case
    when t_cit is null
      let int_flag=0
      construct query1 on expogrp.* from exgp_rec2.*
      if int_flag <> 0 then return end if
      let select1 = "select * from expogrp where ",
        query1 clipped, " order by egcnumb, eglink"
      let select2 = "select count(*) from expogrp where ",
        query1 clipped
      exit case
    otherwise
      let select1 = "select * from expogrp where ",
        "egcnumb = ",quote, t_cit, quote,
        " order by egcnumb, eglink"
      let select2 = "select count(*) from expogrp where ",
        "egcnumb = ",quote, t_cit, quote
      exit case
    end case
  prepare select_exgp from select1
  prepare cnt_exgp from select2
  display "" at 21,2
  display " Searching . . . " at 21,2 attribute(reverse)
  declare cnt_curs cursor for cnt_exgp
  foreach cnt_curs into cnt
    end foreach
  declare eg_curs scroll cursor for select_exgp
  open eg_curs
  call view_exgp()
  close eg_curs
END FUNCTION
#####
FUNCTION vlow_exgp()
  fetch first eg_curs into T_expogrp.*
  if status = NOTFOUND
    then
      MESSAGE "No exposure groups found."
      SLEEP 1
      MESSAGE ""
    else
      let tmp_cnt = 1
      display "" at 21,2
      call disp_exgp()
      display " ", tmp_cnt, " of ", cnt, " rows found." at 21,2
    end if
  MENU "BROWSE"
  COMMAND "Next"
```

```

"View the next Exposure Group in the list." HELP 170
FETCH NEXT eg_curs INTO T_expogrp.*
let tmp_cnt = tmp_cnt + 1
IF status = NOTFOUND THEN
    MESSAGE "No more Exposure Groups in this direction."
    SLEEP 1
    let tmp_cnt = cnt
    MESSAGE ""
    FETCH LAST eg_curs INTO T_expogrp.*
    END IF
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
    attribute(reverse)
call disp_exgp()
COMMAND "Previous"
"View the Previous Exposure Group in the list." HELP 170
FETCH PREVIOUS eg_curs INTO T_expogrp.*
let tmp_cnt = tmp_cnt - 1
IF status = NOTFOUND THEN
    MESSAGE "No more Exposure Groups in this direction."
    SLEEP 1
    MESSAGE ""
    let tmp_cnt = 1
    FETCH FIRST eg_curs INTO T_expogrp.*
    END IF
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
    attribute(reverse)
call disp_exgp()
COMMAND "First"
"View the first Exposure Group in the list." HELP 170
FETCH FIRST eg_curs INTO T_expogrp.*
let tmp_cnt = 1
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
    attribute(reverse)
call disp_exgp()
COMMAND "Last"
"View the Last Exposure Group in the list." HELP 170
message "Searching for last record...."
FETCH LAST eg_curs INTO T_expogrp.*
let tmp_cnt = cnt
message ""
display "" at 21,2
display " ",tmp_cnt, " of ", cnt, " rows" at 21,2
    attribute(reverse)
call disp_exgp()
command "Update"
"Update Exposure Group Link" HELP 171
call update_exgp(T_expogrp.egcitnumb, T_expogrp.egserial)
call disp_exgp()
command "Delete"
"Delete this entry from database" HELP 805
call delete_exgp(T_expogrp.egcitnumb,0,T_expogrp.egserial,1)
call disp_exgp()
command "Query-Again"
"Enter new search criteria" HELP 806

```


Toxin Knowledge System Source Code

```
        close eg_curs
        let citnumber = ""
        call find_exgp(citnumber)
        exit menu
    COMMAND "Exit"
        "Leave this menu" HELP 2
    EXIT MENU
END MENU
end FUNCTION
#####
FUNCTION disp_exgp()
    for x = 11 to 20
        display "" at x,1
    end for
    display by name T_expogrp.*
END FUNCTION
#####
FUNCTION update_exgp(tmp_citnumb, tmp_egserial)
    define
        tmp_citnumb like expogrp.egcitnumb,
        tmp_egserial, hold_serial integer,
        hold_descript like expogrp.egdsgndsc,
        eg, x, y, curr_exgp, exgp_cnt smallint,
        pge integer
    let eg=0
    input
        T_expogrp.egcitnumb,
        T_expogrp.egserial,
        T_expogrp.egdsgnlabel,
        T_expogrp.egsubglabel,
        T_expogrp.egexpolabel,
        T_expogrp.eglink,
        T_expogrp.egtotnum,
        T_expogrp.egdsgndsc,
        T_expogrp.egdsgn,
        T_expogrp.egsubgdsc,
        T_expogrp.egsubg,
        T_expogrp.egexpodsc,
        T_expogrp.egexpo
    without defaults
    from exgp_rec.*
    on key(interrupt)
        let eg=1
        exit input

    after field egcitnumb
        display by name T_expogrp.egcitnumb
        display by name T_expogrp.egtotnum
    before field egdsgnlabel
        call show_dsgn(tmp_citnumb, 0) returning pge
        message "Use CNTL-P to show Previous page, CNTL-N to show Next page"
        on key (CONTROL-P)
            if infield(egdsgnlabel)
                then call show_dsgn(tmp_citnumb, pge-1) returning pge
            end if
        on key (CONTROL-N)
            if infield(egdsgnlabel)
```

```

        then call show_dsgn(tmp_citnumb, pge+1) returning pge
        end if
    after field egdsgnlabel
        call gen_dsgdsc(tmp_citnumb, T_expogrp.egdsgnlabel)
        returning hold_descript, hold_serial
        let T_expogrp.egdsgndsc = hold_descript
        let T_expogrp.egdsgn = hold_serial
        display by name T_expogrp.egdsgndsc
        display by name T_expogrp.egdsgn
    before field egsubglabel
        call show_subj(tmp_citnumb, T_expogrp.egdsgn, 0) returning pge
        message "Use CNTL-P to show Previous page, CNTL-N to show Next page"
        on key (CONTROL-P)
            if infield(egsubglabel) then
                call show_subj(tmp_citnumb, T_expogrp.egdsgn, pge-1) returning pge
            end if
        on key (CONTROL-N)
            if infield(egsubglabel) then
                call show_subj(tmp_citnumb, T_expogrp.egdsgn, pge+1) returning pge
            end if
    after field egsubglabel
        call gen_subdsc(tmp_citnumb,
            T_expogrp.egdsgn,
            T_expogrp.egsubglabel)
        returning hold_descript, hold_serial
        let T_expogrp.egsubgdsc = hold_descript
        let T_expogrp.egsubg = hold_serial
        display by name T_expogrp.egsubgdsc
        display by name T_expogrp.egsubg
    before field egexpolabel
        call show_expo(tmp_citnumb, T_expogrp.egdsgn, 0) returning pge
        message "Use CNTL-P to show Previous page, CNTL-N to show Next page"
        on key (CONTROL-P)
            if infield(egexpolabel) then
                call show_expo(tmp_citnumb, T_expogrp.egdsgn, pge-1) returning pge
            end if
        on key (CONTROL-N)
            if infield(egexpolabel) then
                call show_expo(tmp_citnumb, T_expogrp.egdsgn, pge+1) returning pge
            end if
    after field egexpolabel
        call gen_expdsc(tmp_citnumb,
            T_expogrp.egdsgn,
            T_expogrp.egexpolabel)
        returning hold_descript, hold_serial
        let T_expogrp.egexpodsc = hold_descript
        let T_expogrp.egexpo = hold_serial
        display by name T_expogrp.egexpodsc
        display by name T_expogrp.egexpo
        let T_expogrp.eglink = "D",
            T_expogrp.egdsgnlabel using "<<", "S",
            T_expogrp.egsubglabel using "<<", "E",
            T_expogrp.egexpolabel using "<<"
        display by name T_expogrp.eglink
    end input
    options help key CONTROL-w
    if eg = 1 then return end if

```

Toxin Knowledge System Source Code

```
update expogrp
  set expogrp.* = T_expogrp.*
  where egcitnumb = tmp_citnumb
  and egserial = tmp_egserial
update clinfind
  set cfcitnumb = T_expogrp.egcitnumb,
    cfeglink = T_expogrp.egserial,
    cfeglabel = T_expogrp.eglink
  where cfcitnumb = tmp_citnumb
  and cfeglink = tmp_egserial
END FUNCTION
#####
FUNCTION delete_exgp(tmp_citnumb,tmp_dsgn,tmp_egserial,del_flag)
# del_flag should be 0 to delete without prompt
# del_flag should be 1 to delete with confirmation prompt
# this also handles global deletes from clinfind table
define
  tmp_citnumb,t_cit like expogrp.egcitnumb,
  tmp_egserial,t_eg integer,
  tmp_dsgn,t_dsgn like expogrp.egdsgn,
  del_flag smallint
if del_flag = 0
  then
    case
      when tmp_egserial = 0
        declare del_eg cursor for
          select egcitnumb, egdsgn, egserial
            from expogrp
            where egcitnumb = tmp_citnumb
            and egdsgn = tmp_dsgn
          foreach del_eg into t_cit, t_dsgn, t_eg
            delete from expogrp
              where egcitnumb = t_cit
              and egdsgn = t_dsgn
            delete from clinfind
              where cfcitnumb = t_cit
              and cfeglink = t_eg
          end foreach
        exit case
      when tmp_egserial <> 0
        delete from expogrp
          where egcitnumb = tmp_citnumb
          and egserial = tmp_egserial
        delete from clinfind
          where cfcitnumb = tmp_citnumb
          and cfeglink = tmp_egserial
        exit case
      end case
    else
      call alrt260open()
      prompt "Do you really want to delete this record? (y/N) "
      for answer
        on key(interrupt)
          return
        end prompt
      if upshift(answer) = "Y"
        then
```

```

delete from expogrp
  where egcitrumb = tmp_citrumb
  and egserial = tmp_egserial
select count(*) into x from clinfind
  where cfcitrumb = tmp_citrumb
  and cfeglink = tmp_egserial
if x > 0
  then
    call alrt260p1op()
    message " ", x using "##&"," clinical findings are linked to this."
    prompt "Do you want to delete them? (Y/N) > "
    for answer
    if upshift(answer) = "Y"
      then
        delete from clinfind
          where cfcitrumb = tmp_citrumb
          and cfeglink = tmp_egserial
        message x using "##&"," rows deleted."
        sleep 2
      else
        message "No rows deleted."
        sleep 2
      end if
    end if
    call alrt260p1cl()
  else
    message beep, "No rows deleted"
    sleep 1
  end if
  call alrt260close()
end if
select count(*) into x from expogrp
  where egcitrumb = tmp_citrumb
if status = 0
  then update expogrp set egtotnum = x
    where egcitrumb = tmp_citrumb
  end if
END FUNCTION
#####
FUNCTION renum_exgp(t_cit, t_dsgn, t_sg, t_ex)
# t_dsgn = styserial number# t_sg = sgserial# t_ex = exserial# only one non-zero number permitted
define
  t_cit   like expogrp.egcitrumb,
  t_dsgn, t_sg, t_ex   integer,
  hold_dsgn, hold_sg, hold_ex, hold_eg   integer,
  hold_link   like expogrp.eglink
case
  when t_dsgn != 0
    select stydsgncur into hold_dsgn
      from stydsgn
      where styserial = t_dsgn
    update expogrp
      set egdsgnlabel = hold_dsgn
      where egdsgn = t_dsgn
    declare eg_gen1 cursor for
      select egdsgnlabel, egsubglabell, egexpolabel, egserial
      from expogrp

```

Toxin Knowledge System Source Code

```
        where egcnumb = t_cit
        and egdsgn = t_dsgn
        for update of eglink
    foreach eg_gen1 into hold_dsgn, hold_sg, hold_ex, hold_eg
        let hold_link = "D", hold_dsgn using "<<",
            "S", hold_sg using "<<",
            "E", hold_ex using "<<"
        update expogrp
            set eglink = hold_link
            where current of eg_gen1
        update clinfind
            set cfeglabel = hold_link
            where cfcitnumb = t_cit
            and cfeglink = hold_eg
        end foreach
    exit case
when t_sg != 0
    select sglink into hold_sg
    from subjgrp
    where sgserial = t_sg
    update expogrp
        set egsubglab = hold_sg
        where egsubg = t_sg
    declare eg_gen2 cursor for
        select egdsgnlabel, egsubglab, egexpolabel
        from expogrp
        where egcnumb = t_cit
        and egdsgn = t_sg
        for update of eglink
    foreach eg_gen2 into hold_dsgn, hold_sg, hold_ex
        let hold_link = "D", hold_dsgn using "<<",
            "S", hold_sg using "<<",
            "E", hold_ex using "<<"
        update expogrp
            set eglink = hold_link
            where current of eg_gen2
        update clinfind
            set cfeglabel = hold_link
            where cfcitnumb = t_cit
            and cfeglink = hold_eg
        end foreach
    exit case
when t_ex != 0
    select exlink into hold_ex
    from exporegm
    where exserial = t_ex
    update expogrp
        set egexpolabel = hold_ex
        where egexpo = t_ex
    declare eg_gen3 cursor for
        select egdsgnlabel, egsubglab, egexpolabel
        from expogrp
        where egcnumb = t_cit
        and egdsgn = t_ex
        for update of eglink
    foreach eg_gen3 into hold_dsgn, hold_sg, hold_ex
        let hold_link = "D", hold_dsgn using "<<",
```

```
        "S", hold_sg using "<<",
        "E", hold_ex using "<<"
    update expogrp
        set eglink = hold_link
        where current of eg_gen3
    update clinfind
        set cfeglabel = hold_link
        where cfcitnumb = t_cit
        and cfeglink = hold_eg
    end foreach
    exit case
otherwise
    error "The programmer blew it here!"
    sleep 3
    exit case
end case
end function
```

Toxin Knowledge System Source Code

#tkscfind.4gl

{TITLE: tkscfind.4gl

Copyright, Harold L. Trammel, 1987-1989

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Purpose: to provide entry mechanism for clinical findings

Contains the following FUNCTIONS:

```
    find_control(t_cit)
    add_find(tmp_citnumb)
    find_cfind(t_cit)
    view_cfind()
    disp_cfind(tmp_serial)
    update_cfind(tmp_serial)
    renum_cfind(cf_cit, cf_oldeg, cf_newdeg)
    delete_cfind(cf_serial, cf_flag)
```

}

database tkstest

globals "tksglob.4gl"

#####

FUNCTION flnd_control(t_cit)

define t_cit like clinfind.cfcitnumb

call add_find(t_cit)

END FUNCTION

#####

FUNCTION add_flnd(tmp_citnumb)

define

```
        tmp_sitecode char(8),
        holdsitenum, holdfindnum char(8),
        holdsiteterm, holdfindterm char(70),
        dsgn like expogrp.egdsgndsc,
        subg like expogrp.egsubgdsc,
        expo like expogrp.egexpodsc,
        link like expogrp.eglink,
        tmp_egserial integer,
        tmp_value, tmp_sys char(1),
        tmp_change, t_change like clinfind.cfchange,
        tmp_citnumb, t_cit like clinfind.cfcitnumb,
        tmp_findcode like clinfind.cffindcode,
        tmp_eglink like clinfind.cfeglink
```

call cfwinopen()

let cw=0

let tmp_egserial=0

for cnt = 1 to 50

initialize cf_array[curr_arr].* to null

end for

call set_count(50)

input array cf_array from cf_list.*

on key(interrupt)

let cw =1

exit input

on key(control-p)

case

when infield(cfcitnumb)

```

        let cf_array[curr_arr].cfcitnumb=T_clinfind.cfcitnumb
        next field cfeglink
    when infield(cfeglink)
        let cf_array[curr_arr].cfeglink=T_clinfind.cfeglink
        next field cfsitecode
    when infield(cfsitecode)
        let cf_array[curr_arr].cfsitecode=T_clinfind.cfsitecode
        next field cffindcode
    when infield(cffindcode)
        let cf_array[curr_arr].cffindcode=T_clinfind.cffindcode
        next field cfchange
    when infield(cfchange)
        let cf_array[curr_arr].cfchange=T_clinfind.cfchange
        next field cfsevalue
    when infield(cfsevalue)
        let cf_array[curr_arr].cfsevalue=T_clinfind.cfsevalue
        next field cfseunits
    when infield(cfseunits)
        let cf_array[curr_arr].cfseunits=T_clinfind.cfseunits
        next field cffreq
    when infield(cffreq)
        let cf_array[curr_arr].cffreq=T_clinfind.cffreq
        next field cfonset
    when infield(cfonset)
        let cf_array[curr_arr].cfonset=T_clinfind.cfonset
        next field cfduration
    when infield(cfduration)
        let cf_array[curr_arr].cfduration=T_clinfind.cfduration
        next field cfonset
    end case
before field cfcitnumb
    #initial displays
    message ""
    display "" to egdsgndsc
    display "" to egsubgdsc
    display "" to egexpodsc
    display "" to change
    let curr_arr = arr_curr()
    if curr_arr > 0
        then let T_clinfind.* = cf_array[curr_arr].*
        end if
    if tmp_citnumb is not null
        then
            let cf_array[curr_arr].cfcitnumb = tmp_citnumb
            let cf_array[curr_arr].cfserial = 0
            display by name cf_array[curr_arr].cfcitnumb
            next field cfeglink
        end if
    after field cfcitnumb
        if cf_array[curr_arr].cfcitnumb is null
            then
                error "You must have a CITATION number"
                next field cfcitnumb
            end if
        display by name cf_array[curr_arr].cfcitnumb
        if cf_array[curr_arr].cfcitnumb <> tmp_citnumb
            then

```


Toxin Knowledge System Source Code

```
        let t_cit = cf_array[curr_arr].cfcitnumb
        call exist_citnumb(t_cit) returning x
        if x = 0 then
            error "CITATION data not entered for this number"
            next field cfcitnumb
        end if
    end if
    before field cfeglink
        let tmp_egserial = 0
        message beep, "Press F7 or CNTL-G to see available Exposure Groups"
        on key(F7, control-g)
            if infield(cfeglink)
                then
                    let t_cit = cf_array[curr_arr].cfcitnumb
                    call see_eg(t_cit)
                    returning link, tmp_egserial, dsgn, subg, expo
                    display tmp_egserial to cfeglink
                    display link to cfeglabel
                end if
            after field cfeglink
                if tmp_egserial <> 0
                    then
                        let cf_array[curr_arr].cfeglink = tmp_egserial
                    end if
                    select egdsgndsc, egsubgdsc, egexpodsc, eglink
                    into dsgn, subg, expo, cf_array[curr_arr].cfeglabel
                    from expogrp
                    where egserial = cf_array[curr_arr].cfeglink
                    if status = NOTFOUND then
                        error "No entry for this Exposure Group Number"
                        next field cfeglink
                    end if
                    display by name cf_array[curr_arr].cfeglink
                    display by name cf_array[curr_arr].cfeglabel
                    display dsgn to egdsgndsc
                    display subg to egsubgdsc
                    display expo to egexpodsc
                before field cftype
                    display " M = Pathology Results" at 15,40 attribute(reverse)
                    display " L = Lab/Procedure Results" at 16,40 attribute(reverse)
                    display " S = Signs/Disease Finding" at 17,40 attribute(reverse)
                after field cftype
                    for x = 15 to 17
                        display "" at x,40
                    end for
                    if (cf_array[curr_arr].cftype <> "M" and
                        cf_array[curr_arr].cftype <> "L" and
                        cf_array[curr_arr].cftype <> "S")
                        then
                            error beep, "Wrong choice!"
                            next field cftype
                        end if
                before field cfsitecode
                    let chosen = 0
                    case
                        when cf_array[curr_arr].cftype = "M"
                            call pick_site() returning holdsiter.um, holdsiteterm
```

```

        exit case
    when cf_array[curr_arr].cftype = "L"
        call matrix_choice() returning tmp_value
        call matrix_trans(tmp_value)
        returning holdsitenum, holdsiteterm
    exit case
    when cf_array[curr_arr].cftype = "S"
        call system_choice() returning tmp_value
        call system_trans(tmp_value)
        returning holdsitenum, holdsiteterm
    exit case
    end case
if chosen = 0
    then
        let cf_array[curr_arr].cfsitecode = holdsitenum
        let cf_array[curr_arr].cfsite = holdsiteterm
        display by name cf_array[curr_arr].cfsitecode
        display by name cf_array[curr_arr].cfsite
        next field cffindcode
    else
        next field cftype
    end if
before field cffindcode
    let chosen = 0
    case
        when cf_array[curr_arr].cftype = "M"
            call pick_path()
            returning holdfindnum, holdfindterm
        exit case
        when cf_array[curr_arr].cftype = "L"
            call pick_lab()
            returning holdfindnum, holdfindterm
        exit case
        when cf_array[curr_arr].cftype = "S"
            let tmp_sys = cf_array[curr_arr].cfsitecode clipped
            call pick_sign(tmp_sys)
            returning holdfindnum, holdfindterm
        exit case
    end case
if chosen = 0
    then
        let cf_array[curr_arr].cffindcode = holdfindnum
        let cf_array[curr_arr].cffinding = holdfindterm
        display by name cf_array[curr_arr].cffindcode
        display by name cf_array[curr_arr].cffinding
        next field cfchange
    else
        next field cfsitecode
    end if
before field cfchange
    call change_choice() returning cf_array[curr_arr].cfchange
after field cfchange
    let t_change = cf_array[curr_arr].cfchange
    call trans_change(t_change) returning tmp_change
    display tmp_change to change
    display by name cf_array[curr_arr].cfchange
end input

```

Toxin Knowledge System Source Code

```
if cw = 1 then return end if
for x = 1 to arr_count()
    insert into clinfind values(cf_array[x].*)
end for
END FUNCTION
#####
FUNCTION find_cfInd(t_cit)
    define
        t_cit like clinfind.cfcitnumb
    call cfwinopen()
    let int_flag=0
    construct query1
        on
            cfcitnumb,
            cfsitecode,
            cfsite,
            cffindcode,
            cffinding,
            cfeglink,
            cfchange,
            cfsevvalue,
            cfsevunits,
            cffreq,
            cfonset,
            cfduration
        from
            cfcitnumb,
            cfsitecode,
            cfsite,
            cffindcode,
            cffinding,
            cfeglink,
            cfchange,
            cfsevvalue,
            cfsevunits,
            cffreq,
            cfonset,
            cfduration
    if int_flag <> 0 then return end if
    let select1 = "select * from clinfind where ",
        query1 clipped, " order by cfcitnumb, cfeglink"
    let select2 = "select count(*) from clinfind where ", query1 clipped
    prepare select_cfInd from select1
    prepare cnt_cfInd from select2
    display "" at 20,2
    display "Searching . . ." at 20,2 attribute(reverse)
    declare cnt_curs cursor for cnt_cfInd
    foreach cnt_curs into cnt end foreach
    declare cf_curs scroll cursor for select_cfInd
    open cf_curs
    call view_cfInd()
    close cf_curs
END FUNCTION
#####
FUNCTION view_cfInd()
    fetch first cf_curs into T_clinfind.*
    if status = NOTFOUND
```

```

then
  MESSAGE "No clinical findings found."
  SLEEP 1
  MESSAGE ""
else
  let tmp_cnt = 1
  call disp_cfind(T_clinfind.cfserial)
  display "" at 20,2
  display " ", tmp_cnt, " of ", cnt, " rows found." at 20,2
end if
MENU "BROWSE"
COMMAND "Next"
  "View the next Clinical Finding in the list." HELP 170
  FETCH NEXT cf_curs INTO T_clinfind.*
  let tmp_cnt = tmp_cnt + 1
  IF status = NOTFOUND THEN
    MESSAGE "No more Clinical Findings in this direction."
    SLEEP 1
    let tmp_cnt = cnt
    MESSAGE ""
    FETCH LAST cf_curs INTO T_clinfind.*
    END IF
  display "" at 20,2
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,2
  attribute(reverse)
  call disp_cfind(T_clinfind.cfserial)
COMMAND "Previous"
  "View the Previous Clinical Finding in the list." HELP 170
  FETCH PREVIOUS cf_curs INTO T_clinfind.*
  let tmp_cnt = tmp_cnt - 1
  IF status = NOTFOUND THEN
    MESSAGE "No more Clinical Findings in this direction."
    SLEEP 1
    MESSAGE ""
    let tmp_cnt = 1
    FETCH FIRST cf_curs INTO T_clinfind.*
    END IF
  display "" at 20,2
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,2
  attribute(reverse)
  call disp_cfind(T_clinfind.cfserial)
COMMAND "First"
  "View the first Clinical Finding in the list." HELP 170
  FETCH FIRST cf_curs INTO T_clinfind.*
  let tmp_cnt = 1
  display "" at 20,2
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,2
  attribute(reverse)
  call disp_cfind(T_clinfind.cfserial)
COMMAND "Last"
  "View the Last Clinical Finding in the list." HELP 170
  message "Searching for last record...."
  FETCH LAST cf_curs INTO T_clinfind.*
  let tmp_cnt = cnt
  message ""
  display "" at 20,2
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,2

```

Toxin Knowledge System Source Code

```
        attribute(reverse)
        call disp_cfind(T_clinfind.cfserial)
COMMAND "Update"
    "Update Clinical Finding" HELP 171
    call update_cfind(T_clinfind.cfserial)
COMMAND "Delete"
    "Delete this entry from database" HELP 1003
    call delete_cfind(T_clinfind.cfserial,0)
COMMAND "Query-Again"
    "Enter new search criteria" HELP 1004
    close cf_curs
    let citnumber = ""
    call find_cfind(citnumber)
    exit menu
COMMAND "Exit" "Leave this menu" HELP 2
    close cf_curs
    EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION disp_cfind(tmp_serial)
    define
        tmp_aim char(20),
        dsgn like expogrp.egdsgndsc,
        subg like expogrp.egsubgdsc,
        expo like expogrp.egexpodsc,
        tmp_serial integer,
        x s.nallint
    display by name T_clinfind.*
    # need clinfind change translation call here
    select egdsgndsc, egsubgdsc, egexpodsc
        into dsgn, subg, expo
        from expogrp
        where egserial = T_clinfind.cfeglink
    display dsgn to egdsgndsc
    display subg to egsubgdsc
    display expo to egexpodsc
    END FUNCTION
#####
FUNCTION update_cfind(tmp_serial)
    define
        tmp_sitecode char(8),
        holdsitenum, holdfindnum c (8),
        holdsitenum, holdfindterm char(70),
        dsgn like expogrp.egdsgndsc,
        subg like expogrp.egsubgdsc,
        expo like expogrp.egexpodsc,
        link like expogrp.eglink,
        tmp_egserial, tmp_serial integer,
        tmp_value, tmp_sys char(1),
        tmp_change like clinfind.cfchange,
        tmp_citnumb like clinfind.cfcitnumb,
        tmp_findcode like clinfind.cffindcode,
        tmp_eglink like clinfind.cfeglink
    let cvv=0
    let tmp_citnumb = T_clinfind.cfcitnumb
    input T_clinfind.*
```

```

without defaults from cf_list.*
on key(interrupt)
  let cw = 1
  exit input
before field cfcitnumb
  message ""
  display "" to egdsgndsc
  display "" to egsubgdsc
  display "" to egexpodsc
  display "" to change
  display by name T_clinfind.cfcitnumb
after field cfcitnumb
  if T_clinfind.cfcitnumb is null
    then
      error "You must have a CITATION number"
      next field cfcitnumb
    end if
  if T_clinfind.cfcitnumb <> tmp_citnumb
    then
      call exist_citnumb(T_clinfind.cfcitnumb) returning x
      if x = 0
        then
          error "CITATION data not entered for this number"
          next field cfcitnumb
        end if
      end if
  before field cfeglink
    message beep, "Press F7 or CNTL-G to see available Exposure Groups"
    on key(F7, control-g)
      if infield(cfeglink)
        then
          call see_eg(T_clinfind.cfcitnumb)
            returning link, tmp_egserial, dsgn, subg, expo
          display tmp_egserial to cfeglink
          display link to cfeglabel
        end if
      after field cfeglink
        if tmp_egserial <> 0 then
          let T_clinfind.cfeglink = tmp_egserial
          end if
        select egdsgndsc, egsubgdsc, egexpodsc, eglink
          into dsgn, subg, expo, T_clinfind.cfeglabel
          from expogrp
          where egserial = T_clinfind.cfeglink
        if status = NOTFOUND then
          error "No entry for this Exposure Group Number"
          next field cfeglink
        end if
        display by name T_clinfind.cfeglink
        display by name T_clinfind.cfeglabel
        display dsgn to egdsgndsc
        display subg to egsubgdsc
        display expo to egexpodsc
      before field cftype
        display " M = Pathology Results" at 15,40 attribute(reverse)
        display " L = Lab/Procedure Results" at 16,40 attribute(reverse)
        display " S = Signs/Disease Finding" at 17,40 attribute(reverse)

```

Toxin Knowledge System Source Code

```
after field cftype
  for x = 15 to 17
    display "" at x,40
  end for
  if (T_clinfind.cftype <> "M" and
    T_clinfind.cftype <> "L" and
    T_clinfind.cftype <> "S")
    then
      error beep,"Wrong choice!"
      next field cftype
    end if
before field cfsitecode
  case
    when T_clinfind.cftype = "M"
      call pick_site() returning holdsitenum, holdsiteterm
      exit case
    when T_clinfind.cftype = "L"
      call matrix_choice() returning tmp_value
      call matrix_trans(tmp_value)
      returning holdsitenum, holdsiteterm
      exit case
    when T_clinfind.cftype = "S"
      call system_choice() returning tmp_value
      call system_trans(tmp_value)
      returning holdsitenum, holdsiteterm
      exit case
    end case
  if chosen = 0
    then
      let T_clinfind.cfsitecode = holdsitenum
      let T_clinfind.cfsite = holdsiteterm
      display by name T_clinfind.cfsitecode
      display by name T_clinfind.cfsite
      next field cffindcode
    else
      next field cftype
    end if
before field cffindcode
  case
    when T_clinfind.cftype = "M"
      call pick_path()
      returning holdfindnum, holdfindterm
      exit case
    when T_clinfind.cftype = "L"
      call pick_lab()
      returning holdfindnum, holdfindterm
      exit case
    when T_clinfind.cftype = "S"
      let tmp_sys = T_clinfind.cfsitecode
      call pick_sign(tmp_sys[1])
      returning holdfindnum, holdfindterm
      exit case
    end case
  If chosen = 0
    then
      let T_clinfind.cffindcode = holdfindnum
      let T_clinfind.cffinding = holdfindterm
```

```

        display by name T_clinfind.cffindcode
        display by name T_clinfind.cffinding
        next field cfchange
    else
        next field cffindcode
    end if
before field cfchange
    call change_choice() returning T_clinfind.cfchange
after field cfchange
    call trans_change(T_clinfind.cfchange) returning tmp_change
    display tmp_change to change
    display by name T_clinfind.cfchange
end input
if cw = 1 then return end if
update clinfind
    set clinfind.* = T_clinfind.*
    where cfserial = tmp_serial
END FUNCTION
#####
FUNCTION renum_cfnd(cf_cit, cf_oldeg, cf_neweg)
# renumbers the eglinks after deletes or updates of eglink
# currently this is managed by renum_exgp() in tksexpgrp.4gl
define
    cf_cit like clinfind.cfcitnumb,
    cf_oldeg, cf_neweg like clinfind.cfeglink
update clinfind
    set cfeglink = cf_neweg
    where cfcitnumb = cf_cit
    and cfeglink = cf_oldeg
END FUNCTION
#####
FUNCTION delete_cfnd(cf_serial, cf_flag)
# to delete all cfnds for a given eglink, cf_flag = 0
# otherwise pass through the actual cf_flag, cf_serial
define
    cf_serial integer,
    cf_flag smallint
if cf_flag = 0
    then
        delete from clinfind
            where cfserial = cf_serial
    else
        call alrt260open()
        prompt "Are you sure you want to delete this record? (y/N) "
        for answer
            if upshift(answer) = "Y"
                then
                    delete from clinfind
                        where cfserial = cf_serial
                else
                    message "No row deleted."
                    sleep 1
                end if
            call alrt260close()
        end if
    END FUNCTION

```


Toxin Knowledge System Source Code

#tkscfget.4gl

(TITLE: tkscfget.4gl

Copyright, Harold L. Trammel, 1987-1989

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD 17-C-7114

Purpose: to provide selection mechanism for clinical findings from controlled clinical vocabulary

Contains the following functions:

```
pick_path()
pick_lab()
pick_sign(tmp_sys)
pick_site()
see_organ(tmp_sys)
see_locate(tmp_sys, tmp_org)
see_eg(tmp_cit)
)
database tkstest
globals "tksglob.4gl"
#####
FUNCTION pick_path()
define
    T_path record
        morphcode like morphsynlst.morphcode,
        morphname like morphsynlst.morphsyn
    end record
call synwinopen()
let int_flag = 0
construct query1 on morphsyn from finding
if int_flag <> 0 then return end if
let select1 = "Select morphcode, morphsyn from morphsynlst where ",
    query1 clipped
prepare find_morph from select1
display "Searching...." at 21,2
declare morph_curs cursor for find_morph
let counter = 1
foreach morph_curs into msyn_array[counter].*
    let counter = counter + 1
    if counter > 50 then exit foreach end if
end foreach
case
    when counter = 1
        message "No rows found" attribute(reverse)
        sleep 2
        # need something better to handle no find's
        let chosen = 1
        let T_path.morphcode = "null"
        let T_path.morphname = "null"
        exit case
    when counter = 2
        let T_path.* = msyn_array[1].*
        exit case
    otherwise
        call set_count(counter - 1)
        display array msyn_array to holder.*
        on key(interrupt)
            exit display
        end display
```

```

        let counter = arr_curr()
        let T_path.* = msyn_array[counter].*
        exit case
    end case
    select morphterm into T_path.morphname
    from morphlst
    where morphnum = T_path.morphcode
    call synwinclose()
    return T_path.morphcode, T_path.morphname
END FUNCTION
#####
FUNCTION pick_lab()
    define
        T_lab record
            labcode like labsynlst.labcode,
            labname like labsynlst.labsyn
        end record,
        tmp_sys char(1)
    call synwinopen()
    call labCatChoice() returning tmp_sys
    let int_flag = 0
    construct query1 on labsyn from finding
    if int_flag <> 0 then return end if
    let select1 = "Select labcode, labsyn from labsynlst where ",
        query1 clipped, " and labsynsys = ", quote, tmp_sys, quote
    prepare find_lab from select1
    display "Searching...." at 21,2
    declare lab_curs cursor for find_lab
    let counter = 1
    foreach lab_curs into lsyn_array[counter].*
        let counter = counter + 1
        if counter > 50 then exit foreach end if
    end foreach
    case
        when counter = 1
            message "No rows found" attribute(reverse)
            sleep 2
            # need something better to handle no find's
            let chosen = 1
            let T_lab.labcode = "null"
            let T_lab.labname = "null"
            exit case
        when counter = 2
            let T_lab.* = lsyn_array[1].*
            exit case
        otherwise
            call set_count(counter - 1)
            display array lsyn_array to holder.*
            on key(interrupt)
                exit display
            end display
            let counter = arr_curr()
            let T_lab.* = lsyn_array[counter].*
            exit case
    end case
    select labterm into T_lab.labname
    from lablst

```

Toxin Knowledge System Source Code

```
    where labnum = T_lab.labcode
    call synwinclose()
    return T_lab.labcode, T_lab.labname
END FUNCTION
#####
FUNCTION pick_sign(tmp_sys)
    define
        T_sign record
            signcode like signsynlst.signcode,
            signname like signsynlst.signsyn
        end record,
        tmp_sys char(1)
    call synwinopen()
    let int_flag = 0
    construct query1 on signsyn from finding
    if int_flag <> 0 then return end if
    let select1 = "Select signcode, signsyn from signsynlst where ",
        " signsynsys = ", quote, tmp_sys, quote, " and ", query1 clipped
    prepare find_sign from select1
    display "Searching..." at 21,2
    declare sign_curs cursor for find_sign
    let counter = 1
    foreach sign_curs into ssyn_array[counter].*
        let counter = counter + 1
        if counter > 50 then exit foreach end if
    end foreach
    case
        when counter = 1
            message "No rows found" attribute(reverse)
            sleep 2
            # need something better to handle no find's
            let chosen = 1
            let T_sign.signcode = "null"
            let T_sign.signname = "null"
            exit case
        when counter = 2
            let T_sign.* = ssyn_array[1].*
            exit case
        otherwise
            call set_count(counter - 1)
            display array ssyn_array to holder.*
            on key(interrupt)
                exit display
            end display
            let counter = arr_curr()
            let T_sign.* = ssyn_array[counter].*
            exit case
        end case
    select sign into T_sign.signname
    from signlst
    where signnum = T_sign.signcode
    call synwinclose()
    return T_sign.signcode, T_sign.signname
END FUNCTION
#####
FUNCTION pick_site()
    define
```

```

T_site record
  sys char(1),
  org char(3),
  loc char(5),
  sitecode like tkssite.sitecode,
  locatename like tkssite.locatename
end record,
tmp_value char(1),
tmp_systemname like tkssite.systemname,
tmp_organname like tkssite.organname
open window picksite at 3,3 with form "tkssite"
attribute(border, reverse)
input T_site.* from inputer.*
  before field sys
    call system_choice() returning tmp_value
    call system_trans(tmp_value)
    returning T_site.sys, tmp_systemname
    message "Press RETURN to select Organ or Organ Group."
  after field sys
    display by name T_site.sys
    display tmp_systemname to choicename
    message ""
    call see_organ(T_site.sys) returning T_site.org, tmp_organname
    message "Press RETURN to select Specific Organ Site."
  after field org
    display by name T_site.org
    display tmp_organname to choicename
    message ""
    call see_locate(T_site.sys, T_site.org)
    returning T_site.loc, T_site.locatename
    message "Press RETURN to create Site Code."
  after field loc
    display by name T_site.loc
    display T_site.locatename to choicename
    message "Press ESC to main module."
    let T_site.sitecode = T_site.sys clipped, T_site.loc clipped
    display T_site.sitecode to choice
  end input
close window picksite
return T_site.sitecode, T_site.locatename
END FUNCTION
#####
FUNCTION see_organ(tmp_sys)
define
  tmp_sys char(1),
  holdcode like tkssite.organcode,
  holdname like tkssite.organname,
  list_org ARRAY[50] of record
    code like tkssite.organcode,
    organ like tkssite.organname
  end record
declare see_organ cursor for
  select organcode, organname from tkssite
  where systemcode = tmp_sys
  and locatecode = ""
  order by 1
display "" at 21,3

```

Toxin Knowledge System Source Code

```
display "Searching ..." at 21,3
let counter = 1
foreach see_organ into list_org[counter].*
    let counter = counter + 1
    if counter > 50 then exit foreach end if
end foreach
display "Use arrows to scroll up and down.Press ESC to select item." at 21,3
call set_count(counter -1)
display array list_org to holder.*
let counter = arr_curr()
let holdcode = list_org[counter].code
let holdname = list_org[counter].organ
return holdcode, holdname
END FUNCTION
#####
FUNCTION see_locate(tmp_sys, tmp_org)
define
    tmp_sys char(1),
    tmp_org char(3),
    holdcode like tkssite.locatecode,
    holdname like tkssite.locatename,
    list_loc ARRAY[50] of record
        code like tkssite.locatecode,
        locate like tkssite.locatename
    end record
declare see_locate cursor for
    select locatecode, locatename from tkssite
    where systemcode = tmp_sys
    and organcode = tmp_org
    order by 1
display "" at 21,3
display "Searching ..." at 21,3
let counter = 1
foreach see_locate into list_loc[counter].*
    let counter = counter + 1
    if counter > 50 then exit foreach end if
end foreach
display "Use arrows to scroll up and down.Press ESC to select item." at 21,3
call set_count(counter -1)
display array list_loc to holder.*
let counter = arr_curr()
let holdcode = list_loc[counter].code
let holdname = list_loc[counter].locate
return holdcode, holdname
END FUNCTION
#####
FUNCTION see_eg(tmp_ct)
define
    tmp_ct like expogrp.egcitnumb,
    T_eg record like expogrp.*,
    eg_array ARRAY[20] of record
        eglink like expogrp.eglink,
        egserial like expogrp.egserial,
        egdsgndsc like expogrp.egdsgndsc,
        egsubgdsc like expogrp.egsubgdsc,
        egexpodsc like expogrp.egexpodsc
    end record,
```

```

    holdlink like expogrp.eglink,
    holdserial like expogrp.egserial,
    holddsgn like expogrp.egdsgndsc,
    holdsubg like expogrp.egsubgdsc,
    holdexpo like expogrp.egexpodsc
declare eg_curs cursor for
    select * from expogrp
    where egcitnumb = tmp_cit
    if status = NOTFOUND
        then return 0,0,0,0
    end if
let counter = 1
foreach eg_curs into T_eg.*
    let eg_array[counter].eglink = T_eg.eglink
    let eg_array[counter].egserial = T_eg.egserial
    let eg_array[counter].egdsgndsc = T_eg.egdsgndsc
    let eg_array[counter].egsubgdsc = T_eg.egsubgdsc
    let eg_array[counter].egexpodsc = T_eg.egexpodsc
    let counter = counter + 1
    if counter > T_eg.egtotnum then exit foreach end if
end foreach
open window see_eg at 5,12 with form "tkseg2"
    attribute (border)
display "Use arrows to scroll up and down.Press ESC to select item" at 18,3
call set_count( counter -1)
display by name T_eg.egtotnum, T_eg.egcitnumb
display array eg_array to exgp_rec.*
let counter = arr_curr()
let holdlink=eg_array[counter].eglink
let holdserial=eg_array[counter].egserial
let holddsgn=eg_array[counter].egdsgndsc
let holdsubg=eg_array[counter].egsubgdsc
let holdexpo=eg_array[counter].egexpodsc
close window see_eg
return holdlink, holdserial, holddsgn, holdsubg, holdexpo
END FUNCTION

```

Toxin Knowledge System Source Code

#tksmn1.4gl

```
{
TITLE: tksmonog1.4gl
Copyright, 1987-1988 University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
Contains the following functions:
    single_mono()
    out_mono(c_num)
}
```

```
database tkstest
globals "tksglob.4gl"
```

#####

```
FUNCTION report_cntl()
    MENU "TKS-MONO"
        COMMAND "Abstract"
            "Generate a Structured Abstract for a Given Citation"
            call single_mono()
        COMMAND "Generic"
            "Generate a Monograph for a Given Generic"
            call generic_mono()
        COMMAND "Bibliography"
            "Generate a list of papers in TKS database"
            call biblio_list()
        COMMAND "Exit"
            EXIT MENU
    END MENU
END FUNCTION
```

#####

```
FUNCTION single_mono()
    define
        t_cit    like citation.citnumb
    menu "PAPER-ABSTRACT"
        COMMAND "Generate"
            "Generate a new monograph for a single paper" HELP 1
            call select_src() returning t_cit
            if t_cit is null
                then return
            end if
            clear screen
            display "Preparing Monograph..." at 10, 20
                attribute(reverse)
            call out_mono(t_cit)
            clear screen
            run "less mnggrph.out"
        COMMAND "Print"
            "Print hard copy of current monograph" HELP 1
            clear screen
            display "Printing Output Now..." at 10, 20
                attribute(reverse)
            run "print mnggrph.out"
        COMMAND "Read-Again"
            "View current monograph on-screen" HELP 1
            clear screen
            run "less mnggrph.out"
```

```

COMMAND "Exit" HELP 2
    exit menu
end menu
END FUNCTION
#####
FUNCTION generic_mono()
define
    tmp_val  char(1),
    tmp_gen  like exporegm.exagent,
    runfile  char(50)
menu "GENERIC-MONO"
    COMMAND "Generate"
        "Generate a new monograph for a single generic" HELP 1
        clear screen
        call alrt260open()
        MENU "This will take awhile to generate"
            command "Continue"
                clear window alrt250
                call select_generic() returning tmp_gen
                call genMonoOpt() returning tmp_val
                if tmp_val = "Z"
                    then
                        exit menu
                    else
                        clear window alrt260
                        display "Preparing Monograph ...." at 2,2
                        call genMonoGen(tmp_val, tmp_gen)
                    end if
                let runfile = "less ", outfile
                run runfile
                exit menu
            command "Quit"
                exit menu
        end menu
        call alrt260close()
    COMMAND "Print"
        "Print hard copy of current monograph" HELP 1
        clear screen
        display "Printing Output Now..." at 10,20
        attribute(reverse)
        let runfile = "print ", outfile
        run runfile
    COMMAND "Read-Again"
        "View current monograph on-screen" HELP 1
        clear screen
        let runfile = "less ", outfile
        run runfile
    COMMAND "Exit" HELP 2
        exit menu
end menu
END FUNCTION
-
#####
FUNCTION biblio_list()
define
    tmp_cit like citation.citnumb,
    tmp_auth like authors.authname,
    tmp_gen  like exporegm.exagent

```


Toxin Knowledge System Source Code

```
menu "BIBLIOGRAPHY"
  COMMAND "Total TKS"
    "Generate a comprehensive bibliography of TKS records"
  MENU "TOTAL-TKS"
    COMMAND "Generate"
      "Generate a new bibliography" HELP 1
      call alrt260open()
      MENU "This will take awhile to generate"
        command "Continue"
          display "Preparing bibliography ...." at 2,2
          let outfile = "tottks.out"
          declare bib_gen cursor for
            select citnumb, authname
              from citation, authors
              where authsig = 1
              and citnumb = aucitnumb
              order by 2, 1
          start report bib_out to outfile
          foreach bib_gen into tmp_cit, tmp_auth
            output to report bib_out (tmp_cit, tmp_auth)
          end foreach
          finish report bib_out
          exit menu
        command "Quit"
          exit menu
      end menu
      call alrt260close()
    COMMAND "Print"
      "Print hard copy of current bibliography" HELP 1
      run "print tottks.out"
    COMMAND "Read-Again"
      "View current bibliography on-screen" HELP 1
      run "less tottks.out"
    COMMAND "Exit" HELP 2
      exit menu
  end menu
COMMAND "Author"
  "Generate a comprehensive bibliography for a given author"
  MENU "AUTHOR-TKS"
    COMMAND "Generate"
      "Generate a new bibliography" HELP 1
      call alrt260open()
      prompt "Enter last name and initials >"
      for tmp_auth
        let tmp_auth = upshift(tmp_auth)
      MENU "This will take awhile to generate"
        command "Continue"
          display "Preparing bibliography ...." at 2,2
          let outfile = "authtks.out"
          declare auth_gen cursor for
            select aucitnumb, authname
              from authors
              where authname = tmp_auth
              order by 2,1
          start report bib_out to outfile
          foreach auth_gen into tmp_cit, tmp_auth
            output to report bib_out (tmp_cit, tmp_auth)
```

```

        end foreach
        finish report bib_out
        exit menu
    command "Quit"
        exit menu
    end menu
    call alrt260close()
COMMAND "Print"
    "Print hard copy of current bibliography" HELP 1
    run "print authtks.out"
COMMAND "Read-Again"
    "View current bibliography on-screen" HELP 1
    run "less authtks.out"
COMMAND "Exit" HELP 2
    exit menu
end menu
COMMAND "Generic"
    "Generate a comprehensive bibliography on a given generic"
MENU "GENERIC-TKS"
    COMMAND "Generate"
        "Generate a new bibliography" HELP 1
        call select_generic() returning tmp_gen
        call alrt260open()
        MENU "This will take awhile to generate"
            command "Continue"
                display "Preparing bibliography ...." at 2,2
                let outfile = "generictkts.out"
                declare gen_gen cursor for
                    select unique(excitnumb), authname, exagent
                    from exporegm, authors
                    where exagent = tmp_gen
                    and aucitnumb = excitnumb
                    and authsig = 1
                    order by 2, 1
                start report bib_out to outfile
                foreach gen_gen into tmp_cit, tmp_auth, tmp_gen
                    output to report bib_out (tmp_cit, tmp_auth)
                end foreach
                finish report bib_out
                exit menu
            command "Quit"
                exit menu
            end menu
            call alrt260close()
        COMMAND "Print"
            "Print hard copy of current bibliography" HELP 1
            run "print generictkts.out"
        COMMAND "Read-Again"
            "View current bibliography on-screen" HELP 1
            run "less generictkts.out"
        COMMAND "Exit" HELP 2
            exit menu
        end menu
    COMMAND "Exit"
        exit menu
    END MENU
END FUNCTION

```

Toxin Knowledge System Source Code

#####

FUNCTION out_mono(c_num)

```
define
  c_num like citation.citnumb
  declare out_curs cursor for
    select * from citation
      where citnumb = c_num
    order by citnumb
  start report mono_out to "mngtrph.out"
    foreach out_curs into T_citation.*
      output to report mono_out (T_citation.*)
    end foreach
  finish report mono_out
end FUNCTION
```

#####

REPORT mono_out(c_citation)

```
define
  c_citation record like citation.*,
  tmp_string char(500),
  tmpname char(60),
  author like authors.authname,
  keyword like keywords.keyword,
  aim_str char(20),
  h_dsgnno, h_subjno, h_expono smallint,
  bdwdon, bdwdoff, itwdon, itwdoff char(5)
output
  report to "tks_query.tmp"
  left margin 0
  top margin 0
  bottom margin 0
order external by c_citation.citnumb
format
  before group of c_citation.citnumb
    let citnumber = c_citation.citnumb
  after group of c_citation.citnumb
    #citation information
    print "TKS Citation code: ", c_citation.citnumb
    print "File code: ", c_citation.citfile clipped,
      " in the following files: ", c_citation.citlocate clipped
    call biblio_gen(c_citation.citnumb)
    print bib_entry clipped
    print
    # keyword information
    call keywd_list(c_citation.citnumb)
    print "Keywords Assigned: ", keywdlst clipped
    # paper information
    select count(*) into cnt
      from paperover
      where papcitnumb = citnumber
    if cnt > 0
      then
        print
        print "ABSTRACT"
        print
        # Paper overview information
        print "Overview:"
        call paper_entry(c_citation.citnumb)
```

```

        print pap_string clipped
    # Design information
    print
    print "Design Information:"
    declare dsgn_cur cursor for
        select * into T_stdysgn.*
        from stdysgn
        where stycitnumb = c_citation.citnumb
    foreach dsgn_cur
        print
        print "Design Number ", T_stdysgn.stydsgncur using "<<<"
        call dsgn_entry(c_citation.citnumb)
        print dsgn_string clipped
    # Subject Information
        print
        print "Subject Group Information"
        declare subj_curs cursor for
            select * into T_subjgrp.*
            from subjgrp
            where sgcitnumb = c_citation.citnumb
            and sgdsgnnum = T_stdysgn.styserial
            order by sgdsgnnum
        foreach subj_curs
            print
            print "Subject Group ",
                T_subjgrp.sglink using "<<",
                " of Design ", T_stdysgn.stydsgncur using "<<",";"
            call subj_entry(c_citation.citnumb)
            print subj_string clipped
        end foreach
    close subj_curs
    # Exposure Regimen
    print
    print "Exposure Regimen Information"
    declare expo_curs cursor for
        select * into T_exporegm.*
        from exporegm
        where excitnumb = c_citation.citnumb
        and exdsgnnum = T_stdysgn.styserial
        order by exdsgnnum
    foreach expo_curs
        print
        print "Exposure Regimen ",
            T_exporegm.exlink using "<<",
            " of Design ", T_stdysgn.stydsgncur using "<<",";"
        call expo_entry(c_citation.citnumb)
        print expo_string clipped
    end foreach
    close expo_curs
    end foreach
    end if
# finding/results information
    print
    print "Results: Design-Oriented"
    select count(*) into cnt from clinfind
        where cfcitnumb = c_citation.citnumb
    if cnt < 1

```

Toxin Knowledge System Source Code

```

    then
      print "No clinical findings entered."
      print
      return
    end if
  declare exgp_curs cursor for
  select * from expogrp
  where egcitrnumb = c_citation.citrnumb
  order by egdsgn, egsubg, egexpo
  let h_dsgnno = 0
  let h_subjno = 0
  let h_expono = 0
  foreach exgp_curs into T_expogrp.*
    if T_expogrp.egdsgn <> h_dsgnno
      then
        print 3 spaces, "Design: ", T_expogrp.egdsgndsc clipped
        let h_dsgnno = T_expogrp.egdsgn
      end if
    if T_expogrp.egsubg <> h_subjno
      then
        print 6 spaces, "Subjects: ", T_expogrp.egsubgdsc clipped
        let h_subjno = T_expogrp.egsubg
      end if
    if T_expogrp.egexpo <> h_expono
      then
        print 6 spaces, "Exposure Regimen: ", T_expogrp.egexpodsc clipped
        let h_expono = T_expogrp.egexpo
      end if
  declare find_curs cursor for
  select * from clinfind
  where cfcitrnumb = T_expogrp.egcitrnumb
  and cfeglink = T_expogrp.egserial
  order by cfeglink, cfsitecode, cffinding
  let cnt = 0
  foreach find_curs into T_clinfind.*
    let cnt = cnt + 1
    call find_entry(T_clinfind.cfcitrnumb)
    print find_string clipped
    print
  end foreach
  if cnt = 0
    then
      print "No results reported for this Exposure Group."
      print
    end if
  close find_curs
end foreach
close exgp_curs

end report
#####
REPORT bib_out(c_citation, author)
define
  c_citation like citation.citrnumb;
  tmp_string char(500),
  tmpname char(60),
  author like authors.authname
output

```

```
report to "tks_query.tmp"
left margin 0
top margin 0
bottom margin 0
order external by author, c_citation
format
  first page header
    print "REFERENCES"
    print
  after group of c_citation
    #citation information
    call biblio_gen(c_citation)
    print bib_entry clipped
    print
end report
```

Toxin Knowledge System Source Code

#tksmo2.4gl

```
(
TITLE: tksmon2.4gl
Copyright Harold L. Trammel, 1987-1988
University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
Contains the following functions:
```

```
    biblio_gen(in_cit)
    auth_gen(in_cit)
    auth_down(t_auth)
    keywd_list(in_cit)
    paper_entry(in_cit)
    dsgn_entry(in_cit)
    subj_entry(in_cit)
    expo_entry(in_cit)
    find_entry(in_cit)
)
```

database tkstest

globals "tksglob.4gl"

define

auth_string char(320)

#####

FUNCTION biblio_gen(in_cit)

generates bibliographic entry for a given citation and puts

entry in a global variable 'bib_entry'

define

```
    in_cit like citation.citnumb,
    t_serial integer,
    t_journ like journalst.jabrv,
    t_vol like citation.citvol,
    t_page like citation.citpage,
    t_src like citation.citsource,
    t_date like citation.citdate,
    t_title like citation.cittitle,
    book_record like booklst.*,
    num_string char(10),
    cit_string char(480),
    len smallint
```

call auth_gen(in_cit)

#citation string prep

```
let cit_string = ""
select citserial, citsource, citvol, citpage, citdate, cittitle
into t_serial, t_src, t_vol, t_page, t_date, t_title
from citation
where citnumb = in_cit
if status = NOTFOUND
then
    MESSAGE "No papers found."
    SLEEP 1
    MESSAGE ""
    RETURN
else
    #generate citation
    if t_src[1,1] = "J"
    then
```

```
#####
FUNCTION auth_gen(in_cit)
  define
    in_cit like citation.citnumb,
    t_auth like authors.authname,
    t_asig like authors.authsig,
    aucnt smallint
  let auth_string = ""
  select count(*) into aucnt
  from authors
  where aucitnumb = in_cit
  if status = NOTFOUND
  then
    let auth_string = "Anonymous"
    return
  else
```


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```
declare full_auth cursor for
  select authname, authsig
  from authors
  where aucitnumb = in_cit
  order by 2
foreach full_auth into t_auth, t_asig
  case
    when t_asig > 6
      let auth_string = auth_string clipped, " et al"
      exit foreach
      exit case
    when t_asig = aucnt
      call auth_down(t_auth) returning t_auth
      let auth_string =
        auth_string clipped,
        " ",
        t_auth clipped
      exit case
    when t_asig < aucnt
      call auth_down(t_auth) returning t_auth
      let auth_string =
        auth_string clipped,
        " ",
        t_auth clipped,
        " "
      exit case
    end case
  end foreach
end if
END FUNCTION
#####
FUNCTION auth_down(t_auth)
  define
    t_auth like authors.authname,
    len smallint
  let len = length(t_auth)
  for x = 2 to len
    case
      when t_auth[x,x] = ","
        let t_auth[x,x] = ""
        exit for
        exit case
      when t_auth[x,x] = " "
        let t_auth[x,x] = " "
        exit for
        exit case
      when t_auth[x,x] = "-."
        let x = x+1
        exit case
      otherwise
        let t_auth[x,x] = downshift(t_auth[x,x])
        exit case
    end case
  end for
  return t_auth
END FUNCTION
#####
```

```

FUNCTION keywd_llst(ln_cit)
# generates a string containing the keywords and puts them
# in global variable "keywdlst"
define
  t_key      like keywords.keyword,
  in_cit     like citation.citnumb,
  x, cnt     smallint
select count(*) into cnt
  from keywords
  where keycitnumb = in_cit
if cnt < 1
  then
    let keywdlst = "No keywords entered."
    return
  end if
let x = 0
declare full_keys cursor for
  select keyword from keywords
  where keycitnumb = in_cit
let keywdlst = ""
foreach full_keys into t_key
  let x = x + 1
  if x >= cnt
    then
      let keywdlst = keywdlst clipped, " ",
        downshift(t_key) clipped
      exit foreach
    else
      let keywdlst = keywdlst clipped, " ",
        downshift(t_key) clipped, " ",
    end if
  end foreach
END FUNCTION
#####
FUNCTION paper_entry(ln_cit)
define
  in_cit like paperover.papcitnumb
select * into T_paperover.*
  from paperover
  where papcitnumb = in_cit
let pap_string =
  aim_trans(T_paperover.papaim) clipped,
  " paper with stated purpose of ",
  T_paperover.papstatepur clipped
if length(T_paperover.papimppur) > 0
  then
    let pap_string =
      pap_string clipped,
      " and implied purpose of ",
      T_paperover.papimppur clipped
  end if
let pap_string =
  pap_string clipped, " reporting on ",
  T_paperover.papnumdsgn using "<<<", " design(s)."
END FUNCTION
#####

```

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FUNCTION dsgn_entry(ln_cit)

```
define
  in_cit like citation.citnumb
let dsgn_string =
  "Design Type: ",
  stype_trans(T_stdydsgn.stytype) clipped,
  " experiments were performed in an ",
  vivit_trans(T_stdydsgn.styvivit) clipped,
  " setting with "
case
  when T_stdydsgn.stycntl = "Y"
    let dsgn_string = dsgn_string clipped, " ",
      cntlcmp_trans(T_stdydsgn.stycntcmp) clipped, " ",
      cmpmeth_trans(T_stdydsgn.stycmpmeth) clipped, " ",
      "control(s) using a(n) ",
      cntlmeth_trans(T_stdydsgn.stycntlmeth) clipped, " ",
      cntltyp_trans(T_stdydsgn.stycntltyp) clipped, " ",
      "with ",
      T_stdydsgn.stynumgrp using "<< ", "subject group(s) ",
      cntlassgn_trans(T_stdydsgn.stycntassgn) clipped, " ",
      "assigned to ",
      T_stdydsgn.stynumexp using "<< ", "exposure regimens."
    exit case
  when T_stdydsgn.stycntl = "N"
    let dsgn_string = dsgn_string clipped, " ",
      "no controls using ",
      T_stdydsgn.stynumgrp using "<< ",
      "subject groups and ",
      T_stdydsgn.stynumexp using "<< ",
      "exposure regimens."
    exit case
end case
END FUNCTION
```

#####

FUNCTION subj_entry(ln_cit)

```
define
  in_cit like citation.citnumb
let subj_string =
  "Consisted of ", T_subjgrp.sgnumb using "<<<<<< ", " ",
  sex_trans(T_subjgrp.sgsex) clipped, " ",
  T_subjgrp.sgage clipped, " ",
  date_trans(T_subjgrp.sgageunit) clipped, " old ",
  T_subjgrp.sgbreed clipped, " ",
  T_subjgrp.sgspecies clipped, " weighing ",
  T_subjgrp.sgwt using "<<<<<< ", " kilograms "
if (length(T_subjgrp.sght) > 0 and T_subjgrp.sght <> "NA")
  then
    let subj_string = subj_string clipped, " ",
      T_subjgrp.sght clipped, " ",
      T_subjgrp.sghtunit clipped, " tall"
  end if
if (length(T_subjgrp.sgoccup) > 0 and T_subjgrp.sgoccup <> "NA")
  then
    let subj_string = subj_string clipped, " ",
      " with ", T_subjgrp.sgoccup clipped,
      " occupation "
  end if
```

```

let subj_string = subj_string clipped, " ",
  "of ", T_subjgrp.sghlthstat clipped,
  " health status obtained from ",
  T_subjgrp.sgsources clipped,
  " and received a total of ",
  T_subjgrp.sgtotexpo using "<<<<", " exposure(s)."
END FUNCTION
#####
FUNCTION expo_entry(ln_cit)
define
  in_cit like citation.citnumb
let expo_string = "Involving exposure to ",
  T_exporegm.exagent clipped,
  " for the purpose of assessing ",
  T_exporegm.expurpose clipped,
  " [effects]. It was given by ",
  T_exporegm.exadminmeth clipped,
  " at a dose of ",
  T_exporegm.exdose clipped, " ",
  T_exporegm.exdoseunit clipped, " in a ",
  form_trans(T_exporegm.exformul) clipped, " form by the ",
  rte_trans(T_exporegm.exroute) clipped, " route every ",
  T_exporegm.exinterval clipped, " for a duration of ",
  T_exporegm.exduration clipped, ". "
if (T_exporegm.exevaltime <> "NA"
  or length(T_exporegm.exevaltime) > 0)
then
  let expo_string = expo_string clipped, " ",
    "The subjects were evaluated at ",
    T_exporegm.exevaltime clipped, "."
end if
END FUNCTION
#####
FUNCTION find_entry(ln_cit)
define
  in_cit like citation.citnumb
if length(T_clinfind.cfsevunits) < 1
then
  let find_string =
    severe_trans(T_clinfind.cfsevvalue) clipped, " ",
    trans_change(T_clinfind.cfchange) clipped, " ",
    upshift(T_clinfind.cffinding) clipped, " ",
    "in ", upshift(T_clinfind.cfsite) clipped, " ",
    "seen in ", upshift(T_clinfind.cffreq) clipped,
    " subjects "
  if T_clinfind.cfonset is not null
  then
    let find_string = find_string clipped,
      " with onset of ",
      upshift(T_clinfind.cfonset) clipped, " hour(s) "
  end if
  if T_clinfind.cfduration is not null
  then
    if T_clinfind.cfduration = "CHRONIC"
    then

```

```

        let find_string = find_string clipped,
          " and CHRONIC duration."
      else
        let find_string = find_string clipped,
          " and duration of ",
          upshift(T_clinfind.cfduration) clipped,
          " hour(s)."
      end if
    end if
  else
    let find_string =
      trans_change(T_clinfind.cfchange) clipped, " ",
      upshift(T_clinfind.cffinding) clipped, " ",
      "( ", upshift(T_clinfind.cfsevvalue) clipped, " ",
      upshift(T_clinfind.cfsevunits) clipped, " ) ",
      "in ", upshift(T_clinfind.cfsite) clipped, " ",
      "seen in ", upshift(T_clinfind.cfreq) clipped,
      " subjects "
    if T_clinfind.cfonset is not null
      then
        let find_string = find_string clipped,
          " with onset of ",
          upshift(T_clinfind.cfonset) clipped, " hour(s) "
      end if
    if T_clinfind.cfduration is not null
      then
        if T_clinfind.cfduration = "CHRONIC"
          then
            let find_string = find_string clipped,
              " and CHRONIC duration."
          else
            let find_string = find_string clipped,
              " and duration of ",
              upshift(T_clinfind.cfduration) clipped,
              " hour(s)."
          end if
        end if
      end if
    end if
  END FUNCTION

```

```

#tksmmon3.4gl
{
  TITLE: tksmon3.4gl
  Copyright Harold L. Trammel, 1987-1988
  University of Illinois, CVM, IAPIC
  Funded by US Army Contract DAMD-17-C-7114
  Contains the following functions:

}
database tkstest
globals "tksglob.4gl"
define
  T_generic like exporegm.exagent,
  chem_string char(80),
  outfile3 char(80)
#####
FUNCTION select_generic()
  define
    tmp_gen like exporegm.exagent
    open window a260 at 10,10 with 2 rows, 60 columns
    attribute(border, green)
    prompt "Enter generic >"
    for tmp_gen
      let tmp_gen = upshift(tmp_gen)
    close window a260
    return tmp_gen
  end function
#####
FUNCTION genMonoOpt()
  open window alrt1960 at 4,20 with 19 rows, 60 columns
  attribute (border, green, prompt line last -1)
  display "REPORT CHOICES FOR GENERIC— DEC. 1989" at 1,10
  display "A = System-Sign-Species-Dose-Study Design " at 3,2
  display "B = Species-System-Sign-Dose-Study Design " at 5,2
  display "C = Dose-Species-System-Sign-Study Design " at 7,2
  display "D = Study Design-Species-System-Sign-Dose " at 9,2
  display "T = Total Agent Monograph " at 15,2
  display "Z = Exit " at 17,2
  prompt "Enter report choice > " for char answer
  on key(interrupt)
    let answer = "Z"
    close window alrt1960
    return answer
  end prompt
  let answer = upshift(answer)
  close window alrt1960
  return answer
end function
#####
FUNCTION genMonoGen(tmp_val, tmp_gen)
  define
    tmp_val char(1),
    runfile,outfile2 char(80),
    tmp_gen like exporegm.exagent,
    t_sys char(1),
    t_citnumb like citation.citnumb,

```

```

t_cftype like clinfind.cftype,
t_cffinding like clinfind.cffinding,
t_cfchange like clinfind.cfchange,
t_cfsevvalue like clinfind.cfsevvalue,
t_cfsevunits like clinfind.cfsevunits,
t_cffreq like clinfind.cffreq,
t_cfonset like clinfind.cfonset,
t_cfduration like clinfind.cfduration,
t_egsubgdsc like expogrp.egsubgdsc,
t_egexpodsc like expogrp.egexpodsc,
t_egdsgndsc like expogrp.egdsgndsc,
t_authname like authors.authname,
t_exagent like exporegm.exagent,
t_citserial like citation.citserial,
t_gen char(4)

let t_gen = tmp_gen[1,4]
for x = 1 to 4
  if t_gen[x,x] = " "
    then
      let t_gen[x,x] = "_ "
    end if
  end for
Case
when tmp_val = "A"
  let outfile = t_gen,"mono.out"
  let outfile2 = t_gen,"bib.out"
  let outfile3 = t_gen,".out"
  declare a_curs cursor for
    select
      cftype,
      cfsitecode[1],
      cffinding,
      cfchange,
      cfsevvalue,
      cfsevunits,
      cffreq,
      cfonset,
      cfduration,
      egsubgdsc,
      egexpodsc,
      egdsgndsc,
      citserial
    from clinfind, expogrp, exporegm, citation
    where exagent = tmp_gen
    and egexpo = exserial
    and cfeglink = egserial
    and citnumb = cfcitnumb
    order by 1 desc, 2, 3, 4
  start report genMono to outfile
  foreach a_curs into
    t_cftype, t_sys, t_cffinding, t_cfchange,
    t_cfsevvalue, t_cfsevunits, t_cffreq, t_cfonset,
    t_cfduration, t_egsubgdsc, t_egexpodsc, t_egdsgndsc,
    t_citserial
  output to report genMono(
    t_cftype, t_sys, t_cffinding, t_cfchange,

```

```

        t_cfsevalue,t_cfseunits,t_cffreq,t_cfonset,
        t_cfduration,t_egsubgdsc,t_egexpodsc,t_egdsgndsc,
        t_citserial)
    end foreach
    finish report genMono
close a_curs
declare a_bib cursor for
    select unique(egcitnumb), authname, exagent
    from clinfind, authors, exporegm, expogrp
    where exagent = tmp_gen
    and egexpo = exserial
    and authsig = 1
    and egcitnumb = cfcitnumb
    and egcitnumb = aucitnumb
    and egcitnumb = excitnumb
    order by 2
    start report bib_out to outfile2
    foreach a_bib into t_citnumb, t_authname, t_exagent
        output to report bib_out(t_citnumb, t_authname)
    end foreach
    finish report bib_out
    Close a_bib
    let runfile = "cat ", outfile clipped, " ", outfile2 clipped, ">", outfile3 clipped
    run runfile
    exit case
    when tmp_val = "B"
    when tmp_val = "C"
    when tmp_val = "D"
    when tmp_val = "T"
        call genMonoTot(tmp_gen)
    exit case
end case
end function
#####
REPORT genMono(t_cftype, t_sys, t_cffinding, t_cfchange, t_cfsevalue, t_cfseunits, t_cffreq,
t_cfonset, t_cfduration, t_egsubgdsc, t_egexpodsc, t_egdsgndsc, t_citserial)
define
    tmp_val    char(1),
    tmp_gen    like exporegm.exagent,
    tmp_sys    like tkssite.systemcode,
    tmp_systemname like tkssite.systemname,
    junque char(10),
    t_cftype like clinfind.cftype,
    t_sys char(1),
    t_cffinding like clinfind.cffinding,
    t_cfchange like clinfind.cfchange,
    t_cfsevalue like clinfind.cfsevalue,
    t_cfseunits like clinfind.cfseunits,
    t_cffreq like clinfind.cffreq,
    t_cfonset like clinfind.cfonset,
    t_cfduration like clinfind.cfduration,
    t_egsubgdsc like expogrp.egsubgdsc,
    t_egexpodsc like expogrp.egexpodsc,
    t_egdsgndsc like expogrp.egdsgndsc,
    t_citserial like citation.citserial
output
    left margin 0

```


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```
right margin 0
bottom margin 0
order external by t_cftype, t_sys, t_cffinding, t_cfchange
format
  before group of t_cftype
    case
      when t_cftype = "S"
        print "Signs/Disease"
        print
        exit case
      when t_cftype = "M"
        print "Morphology"
        print
        exit case
      when t_cftype = "L"
        print "Laboratory Findings"
        print
        exit case
    end case
  before group of t_sys
    case
      when t_cftype = "S"
        call system_trans(t_sys) returning junque, tmp_systemname
        exit case
      when t_cftype = "M"
        call system_trans(t_sys) returning junque, tmp_systemname
        exit case
      when t_cftype = "L"
        call matrix_trans(t_sys) returning junque, tmp_systemname
        exit case
    end case
  print tmp_systemname
  before group of t_cffinding
    print 3 spaces, t_cffinding clipped
  on every row
    print trans_change(t_cfchange) clipped. 1 spaces,
      "(, t_cfsevalue clipped,
      t_cfseunits clipped, ") occurring in ",
      t_cffreq clipped, " subjects at ",
      t_cfonset clipped, " with ",
      t_cfduration clipped, " duration. ",
      " Subjects: ", t_egsubgdsc clipped,
      " Exposures: ", t_egexpodsc clipped,
      " Design: ", t_egdsgndsc clipped,
      " (, t_citserial using "<<<<<<," )"
    print
  end report
#####
FUNCTION chem_data(t_gen)
  define t_gen like exporegm.exagent

  let chem_string = "CHEMICAL DATA: None available at this time."
  END FUNCTION
#####
FUNCTION genMonoTot(t_gen)
  define
    t_gen like exporegm.exagent,
```

```

outfile2, runfile char(80),
t_citnumb like citation.citnumb,
t_authname like authors.authname,
t_exagent like exporegm.exagent
t_gen1 char(4)

let t_gen1 = t_gen[1,4]
for x = 1 to 4
  if t_gen1[x,x] = " "
    then
      let t_gen1[x,x] = "_"
    end if
  end for

let outfile = t_gen1,"tot.out"
let outfile2 = t_gen1,"bib.out"
let outfile3 = t_gen1,".out"
let T_generic = t_gen

declare agt_curs cursor for
select
  cfcitnumb,
  cfserial,
  cfeglink,
  cfeglabel,
  cfetype,
  cfsitecode,
  cfsite,
  cffindcode,
  cffinding,
  cfchange,
  cfsevalue,
  cfseunits,
  cffreq,
  cfonset,
  cfduration
from clinfind, exporegm, expogrp
where exporegm.exagent = t_gen
and expogrp.egexpo = exporegm.exserial
and cfeglink = expogrp.egserial
order by cfetype desc, cfsitecode, cffinding, cfchange, cfsevalue
start report totGenMono to outfile
foreach agt_curs into T_clinfind.*
  output to report totGenMono(T_clinfind.*)
end foreach
finish report totGenMono
close agt_curs
declare agt_bib cursor for
select unique(egcitnumb), authname, exagent
from clinfind, authors, exporegm, expogrp
where exagent = t_gen
and egexpo = exserial
and authsig = 1
and egcitnumb = cfcitnumb
and egcitnumb = aucitnumb
and egcitnumb = excitnumb
order by 2

```

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```

start report bib_out to outfile2
  foreach agt_bib into t_citnumb, t_authname, t_exagent
    output to report bib_out(t_citnumb, t_authname)
  end foreach
finish report bib_out
Close agt_bib
let runfile = "cat", outfile clipped, " ", outfile2 clipped, ">", outfile3 clipped
run runfile
end function

```

#####

REPORT totGenMono(c_clinfind)

```

define
  c_clinfind record like clinfind.*,
  t_sys char(1),
  junque char(10),
  t_cftype like clinfind.cftype,
  tmp_systemname like tkssite.systemname,
  tmp_citserial integer
order external by c_clinfind.cftype,
  c_clinfind.cfsitecode,
  c_clinfind.cffinding,
  c_clinfind.cfchange,
  c_clinfind.cfsevalue
format
  first page header
  print t_generic
  print
  call chem_data(t_generic)
  print chem_string
  print
  page header
  print t_generic clipped, " MONOGRAPH — page ",pageno using "<<<<"
  print
  before group of c_clinfind.cftype
  case
    when c_clinfind.cftype = "S"
      print
      print "Signs/Disease"
      exit case
    when c_clinfind.cftype = "M"
      print
      print "Morphology"
      exit case
    when c_clinfind.cftype = "L"
      print
      print "Laboratory Findings"
      exit case
  end case
  before group of c_clinfind.cfsitecode
  let t_sys = c_clinfind.cfsitecode[1]
  case
    when c_clinfind.cftype = "S"
      call system_trans(t_sys) returning junque, tmp_systemname
      exit case
    when c_clinfind.cftype = "M"
      call system_trans(t_sys) returning junque, tmp_systemname

```

```

        exit case
    when c_clinfind.cftype = "L"
        call matrix_trans(t_sys) returning junque, tmp_systemname
    exit case
end case
print
print tmp_systemname
on every row
select * into T_subigrp.*
    from subigrp, expogrp
    where sgserial = egsubg
    and egserial= c_clinfind.cfeglink
select * into T_exporegm.*
    from exporegm, expogrp
    where c_clinfind.cfeglink = egserial
    and exserial = egexpo
select citserial into tmp_citserial
    from citation
    where citnumb = c_clinfind.cfcitnumb
if length(T_clinfind.cfsevunits) < 1
    then
        print
        print
        severe_trans(T_clinfind.cfsevvalue) clipped, " ",
        trans_change(T_clinfind.cfchange) clipped, " ",
        upshift(T_clinfind.cffinding) clipped, " ";
        if T_clinfind.cftype <> "S"
            then
                print "in ", upshift(T_clinfind.cfsite) clipped, " ";
            end if
        print "seen in ", upshift(T_clinfind.cffreq) clipped, " ",
        sex_trans(T_subigrp.sgsex) clipped, " ",
        T_subigrp.sgage clipped, " ",
        date_trans(T_subigrp.sgageunit) clipped, " old ",
        T_subigrp.sgbreed clipped, " ",
        T_subigrp.sgspecies clipped, " weighing ",
        T_subigrp.sgmt using "<<<<<", " kilograms ";
        if (length(T_subigrp.sght) > 0 and T_subigrp.sght <> "NA")
            then
                print T_subigrp.sght clipped, " ",
                T_subigrp.sghtunit clipped, " tall";
            end if
        if (length(T_subigrp.sgoccup) > 0 and T_subigrp.sgoccup <> "NA")
            then
                print "with ", T_subigrp.sgoccup clipped,
                " occupation ";
            end if
        print "of ", T_subigrp.sghlthstat clipped,
        " health status (obtained from ",
        T_subigrp.sgsource clipped,
        ") which received a total of ",
        T_subigrp.sgtotexpo using "<<<<<", " exposure(s) to ",
        T_exporegm.exdose clipped, " ",
        T_exporegm.exdoseunit clipped, 1 space,
        T_exporegm.exagent clipped, " by ",
        T_exporegm.exadminmeth clipped, " ",
        rte_trans(T_exporegm.exroute) clipped, " route every ",

```

1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

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```

T_exporegm.exdose clipped, " ",
T_exporegm.exdoseunit clipped, 1 space,
T_exporegm.exagent clipped, " by ",
T_exporegm.exadminmeth clipped, " ",
rte_trans(T_exporegm.exroute) clipped, " route every ",
T_exporegm.exinterval clipped, " for a duration of ",
T_exporegm.exduration clipped, ". ";
if (T_exporegm.exevaltime <> "NA"
    or length(T_exporegm.exevaltime) > 0)
    then
        print " The subjects were evaluated at ",
        T_exporegm.exevaltime clipped, ". ";
    end if
if T_clinfind.cfonsset is not null
    then
        print " Clinical effects had onset of ",
        upshift(T_clinfind.cfonsset) clipped, " ";
    end if
if T_clinfind.cfduration is not null
    then
        if T_clinfind.cfduration = "CHRONIC"
            then
                print " and CHRONIC duration. ";
            else
                print " and duration of ",
                upshift(T_clinfind.cfduration) clipped,
                ". ";
            end if
        print " (", tmp_citserial using "<<<<<<<", ")"
    end if
end if
end report

```

Toxin Knowledge System Source Code

#tksvoc.4gl

{
TITLE: tksvoc.4gl
Copyright Harold L. Trammel, 1987-1988
University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
Contains the following FUNCTIONS:

j_list()
add_journ()
update_journ()
delete_journ()
query_journ()
view_journ()
dispname()
b_list()
add_book()
update_book()
delete_book()
query_book()
view_book()
bdispname()
k_list()
add_klist()
update_klist()
delete_klist()
query_klist()
view_klist()
dispkey()

}
DATABASE tkstest
GLOBALS "tksglob.4gl"
#Journal FUNCTION
FUNCTION j_list()
define
answer char(1)
open window jw1 at 3,3 with form "vocjourn" ATTRIBUTE (BORDER)
menu "JOURNAL-VOCABULARY"
COMMAND "Add"
"Add Journal to Journal Vocabulary" HELP 900
call add_journ()
COMMAND "Find"
"Find Journal in Journal Vocabulary" HELP 901
call query_journ()
COMMAND "Exit"
"Exit from Journal Vocabulary Modification" HELP 2
exit menu
END menu
Close window jw1
clear screen
END FUNCTION
FUNCTION add_journ()
define
jname2 char(60),
jname1 char(60),
jrow integer
MESSAGE ""

```

CLEAR FORM
let sw = 0
INPUT
  jname1, jname2, T_journalst.jabrv
FROM
  jname, jnm, jabrv
ON KEY (INTERRUPT)
  let sw = 1
  EXIT INPUT
END INPUT
IF sw = 1 then RETURN end if
let T_journalst.jacquis = 0
let T_journalst.jcode = "J00000"
let T_journalst.jname = jname1 clipped, jname2
insert into journalst values (T_journalst.*)
let T_journalst.jacquis = SQLCA.SQLERRD[2]
let T_journalst.jcode = "J", T_journalst.jacquis using "&&&&&"
update journalst set jcode = T_journalst.jcode
  where T_journalst.jabrv = journalst.jabrv
display T_journalst.jacquis to jacquis
display T_journalst.jcode to jcode
MESSAGE "Row Added"
sleep 1
MESSAGE ""
END FUNCTION
FUNCTION update_journal()
define
  jname2 char(60),
  jname1 char(60),
  jrow integer
let jname1 = T_journalst.jname[1,60]
let jname2 = T_journalst.jname[61,120]
let sw = 0
INPUT
  T_journalst.jacquis, T_journalst.jcode,
  jname1, jname2,
  T_journalst.jabrv
WITHOUT DEFAULTS
FROM
  jacquis, jcode, jname, jnm, jabrv
ON KEY (INTERRUPT)
  let sw = 1
  EXIT INPUT
END INPUT
IF sw = 1 then RETURN END IF
let T_journalst.jname = jname1 clipped, jname2
UPDATE journalst
  SET journalst.* = T_journalst.*
  where journalst.jcode = T_journalst.jcode
MESSAGE "Row Updated."
SLEEP 1
MESSAGE ""
END FUNCTION
FUNCTION delete_journal()
DELETE FROM journalst WHERE jcode = T_journalst.jcode
CLEAR FORM
MESSAGE "Row Deleted."

```


Toxin Knowledge System Source-Code

```
SLEEP 1
MESSAGE ""
END FUNCTION
FUNCTION query_journ()
  clear form
  let int_flag = 0
  construct query1 on jcode, jname, jabrv
    from journalst.*
  if int_flag <> 0 then return end if
  let select1 = "select * from journalst where ", query1 clipped
  prepare select_2 from select1
  let select2 = "select count(*) from journalst where ", query1 clipped
  prepare jor_cnt from select2
  declare jor_curs cursor for jor_cnt
  foreach jor_curs into cnt end foreach
  declare j_curs SCROLL CURSOR FOR select_2
  let chosen = FALSE
  OPEN j_curs
  MESSAGE " Searching... "
  FETCH FIRST j_curs into T_journalst.*
  IF status = NOTFOUND
    THEN
      MESSAGE "No Journal Found"
      SLEEP 1
      MESSAGE ""
    ELSE
      display " ", cnt, " rows found" at 17,2 attribute(reverse)
      CALL view_journ()
    END IF
  CLOSE j_curs
END FUNCTION
FUNCTION view_journ()
  CALL dispname()
  let tmp_cnt = 1
  display "" at 17,2
  display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
  MENU "BROWSE"
  COMMAND "Next"
    "View the next Journal in the list." HELP 170
    FETCH NEXT j_curs INTO T_journalst.*
    let tmp_cnt = tmp_cnt + 1
    IF status = NOTFOUND THEN
      MESSAGE "No more Journals in this direction."
      SLEEP 1
      let tmp_cnt = cnt
      MESSAGE ""
      FETCH LAST j_curs INTO T_journalst.*
      END IF
    display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
    attribute(reverse)
    call dispname()
  COMMAND "Previous"
    "View the Previous Journal in the list." HELP 170
    FETCH PREVIOUS j_curs INTO T_journalst.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
      MESSAGE "No more Journals in this direction."
```

```

        SLEEP 1
        MESSAGE ""
        let tmp_cnt = 1
        FETCH FIRST j_curs INTO T_journalst.*
        END IF
        display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
        attribute(reverse)
        call dispname()
    COMMAND "First"
        "View the first Journal in the list." HELP 170
        FETCH FIRST j_curs INTO T_journalst.*
        let tmp_cnt = 1
        display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
        attribute(reverse)
        call dispname()
    COMMAND "Last"
        "View the Last Journal in the list." HELP 170
        message "Searching for last record...."
        FETCH LAST j_curs INTO T_journalst.*
        let tmp_cnt = cnt
        message ""
        display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
        attribute(reverse)
        message ""
        call dispname()
    COMMAND "Update"
        "Update Journal in Journal Vocabulary" HELP 171
        call update_journal()
    COMMAND "Delete"
        "Delete Journal from Journal Vocabulary" HELP 908
        prompt "Are you sure you want to delete this Journal (y/n)? "
        for answer
        IF answer = "y"
            then
                call delete_journal()
            else
                next option "Next"
            END IF
        COMMAND "Exit" "Leave this menu" HELP 2
        EXIT MENU
    END MENU
END FUNCTION
FUNCTION dispname()
    define
        jname1 char(60),
        jname2 char(60)
    let jname1 = T_journalst.jname[1,60]
    let jname2 = T_journalst.jname[61,120]
    display
        T_journalst.jacquis,
        T_journalst.jcode,
        jname1,
        jname2,
        T_journalst.jabrv
    to
        jacquis, jcode, jname, jnm, jabrv
END FUNCTION

```

Toxin Knowledge System Source Code

#Book FUNCTION

FUNCTION b_list()

```
define
  answer char(1)
  open window bw1 at 3,3 with 20 rows, 69 columns ATTRIBUTE (BORDER)
  open form s_book from "vocbook"
  display form s_book
  let chosen = FALSE
  menu "BOOK-VOCABULARY"
    COMMAND "Add"
      "Add Book to Book Vocabulary" HELP 906
      call add_book()
    COMMAND "Find"
      "Find Book in Book Vocabulary" HELP 907
      call query_book()
    COMMAND "Exit"
      "Exit from Book Vocabulary Modification" HELP 2
      exit menu
  END menu
  Close window bw1
  clear screen
END FUNCTION
```

FUNCTION add_book()

```
define
  bname2 char(60),
  bname1 char(60),
  brow integer
MESSAGE ""
CLEAR FORM
let sw = 0
INPUT BY NAME
  T_booklst.bname THRU T_booklst.bisbn
  ON KEY (INTERRUPT)
    let sw = 1
    EXIT INPUT
  END INPUT
IF sw = 1 then RETURN end if
let T_booklst.bacquis = 0
let T_booklst.bcode = "B00000"
insert into booklst values (T_booklst.*)
let T_booklst.bacquis = SQLCA.SQLERRD[2]
let T_booklst.bcode = "B",T_booklst.bacquis using "&&&&&"
update booklst set bcode = T_booklst.bcode
  where booklst.bacquis = T_booklst.bacquis
display T_booklst.bacquis to bacquis
display T_booklst.bcode to bcode
MESSAGE "Row Added"
sleep 1
MESSAGE ""
END FUNCTION
```

FUNCTION update_book()

```
define
  bname2 char(60),
  bname1 char(60),
  brow integer
let sw = 0
INPUT BY NAME
```

```

T_booklst.* WITHOUT DEFAULTS
ON KEY (INTERRUPT)
    let sw = 1
    EXIT INPUT
END INPUT
IF sw = 1 then RETURN end if
UPDATE booklst
    SET booklst.* = T_booklst.*
    where booklst.bcode= T_booklst.bcode
MESSAGE "Row Updated."
SLEEP 1
MESSAGE ""
END FUNCTION
FUNCTION delete_book()
DELETE FROM booklst WHERE bcode= T_booklst.bcode
CLEAR FORM
MESSAGE "Row Deleted."
SLEEP 1
MESSAGE ""
END FUNCTION
FUNCTION query_book()
clear form
let int_flag = 0
construct query1
    on
        bcode, bname, bedno, bvol,
        bdate, bpub,
        bpubplace, beditor, bisbn
    from
        booklst.bcode, booklst.bname, booklst.bedno, booklst.bvol,
        booklst.bdate, booklst.bpub,
        booklst.bpubplace, booklst.beditor, booklst.bisbn
if int_flag <> 0 then return end if
let select1 = "select * from booklst where ", query1 clipped
prepare select_3 from select1
let select2 = "select count(*) from booklst where ", query1 clipped
prepare bk_cnt from select2
declare bk_curs cursor for bk_cnt
foreach bk_curs into cnt
end foreach
declare b_curs SCROLL CURSOR FOR select_3
let chosen = FALSE
OPEN b_curs
MESSAGE " SEARCHING..."
FETCH FIRST b_curs into T_booklst.*
IF status = NOTFOUND
    THEN
        MESSAGE "No Book Four 1"
        SLEEP 1
        MESSAGE ""
    ELSE
        display " ", cnt, " rows found" at 16,2 attribute(reverse)
        CALL bdispname()
        CALL view_book()
    END IF
CLOSE b_curs
END FUNCTION

```

Toxin Knowledge System Source Code

```
FUNCTION view_book()
  let tmp_cnt = 1
  display "" at 16,2
  MENU "BROWSE"
    COMMAND "Next"
      "View the next Book in the list." HELP 170
      FETCH NEXT b_curs INTO T_booklst.*
      let tmp_cnt = tmp_cnt + 1
      IF status = NOTFOUND THEN
        MESSAGE "No more Books in this direction."
        SLEEP 1
        let tmp_cnt = cnt
        MESSAGE ""
        FETCH LAST b_curs INTO T_booklst.*
      END IF
      display ~ ", tmp_cnt, " of ", cnt, " rows" at 16,2
      attribute(reverse)
      call bdispname()
    COMMAND "Previous"
      "View the Previous Book in the list." HELP 170
      FETCH PREVIOUS b_curs INTO T_booklst.*
      let tmp_cnt = tmp_cnt - 1
      IF status = NOTFOUND THEN
        MESSAGE "No more book in this direction."
        SLEEP 1
        MESSAGE ""
        let tmp_cnt = 1
        FETCH FIRST b_curs INTO T_booklst.*
      END IF
      display ~ ", tmp_cnt, " of ", cnt, " rows" at 16,2
      attribute(reverse)
      call bdispname()
    COMMAND "First" "View the first Book in the list." HELP 170
      FETCH FIRST b_curs INTO T_booklst.*
      let tmp_cnt = 1
      display ~ ", tmp_cnt, " of ", cnt, " rows" at 16,2
      attribute(reverse)
      call bdispname()
    COMMAND "Last" "View the Last Book in the list." HELP 170
      message "Searching for last record...."
      FETCH LAST b_curs INTO T_booklst.*
      let tmp_cnt = cnt
      message ""
      display ~ ", tmp_cnt, " of ", cnt, " rows" at 16,2
      attribute(reverse)
      call bdispname()
    COMMAND "Update" "Update Book in Book Vocabulary" HELP 171
      call bdispname()
      call update_book()
    COMMAND "Delete" "Delete Book from Book Vocabulary" HELP 909
      call bdispname()
      prompt "Are you sure you want to delete this Book (y/n)? "
      for answer
      IF answer = "y"
        then
          call delete_book()
        ELSE
```

```

        NEXT OPTION "Find"
    END IF
    COMMAND "Exit"
        "Leave this menu" HELP 2
    EXIT MENU
END MENU
END FUNCTION
FUNCTION bdispname()
    display
        T_booklst.bacquis,
        T_booklst.bcode,
        T_booklst.bname,
        T_booklst.bedno,
        T_booklst.bvol,
        T_booklst.bdate,
        T_booklst.bpub,
        T_booklst.bpubplace,
        T_booklst.beditor,
        T_booklst.bisbn
    to
        bacquis, bcode, bname, bedno,
        bvol, bdate,
        bpub, bpubplace, beditor, bisbn
END FUNCTION
#Keyword FUNCTION
FUNCTION k_list()
    define
        answer char(1)
    open window kw1 at 10,3 with 10 rows, 66 columns ATTRIBUTE (BORDER)
    open form s_key from "vockeys"
    display form s_key
    menu "KEYWORD_LISTING"
        COMMAND "Add"
            "Add Keyword to Keyword Vocabulary" HELP 903
            call add_klist()
        COMMAND "Find"
            "Find Keyword in Keyword Vocabulary" HELP 904
            call query_klist()
        COMMAND "Exit" "Exit from Keyword Vocabulary Modification" HELP 2
    exit menu
    END menu
    Close window kw1
    clear screen
END FUNCTION
FUNCTION add_klist()
    MESSAGE ""
    CLEAR FORM
    INPUT by name T_keylist.*
    ON KEY (INTERRUPT)
        let sw = 1
        EXIT INPUT
    END INPUT
    if sw = 1 then return end if
    insert into keylist values (T_keylist.*)
    MESSAGE "Row added"
    sleep 1
    MESSAGE ""

```

Toxin Knowledge System Source Code

```
END FUNCTION
FUNCTION update_klist()
  define
    tmp_code like keylist.kcode
  let tmp_code = T_keylist.kcode
  INPUT by name T_keylist.* WITHOUT DEFAULTS
    ON KEY (INTERRUPT)
      EXIT INPUT
    END INPUT
  UPDATE keylist
    SET keylist.* = T_keylist.*
    where keylist.kcode= tmp_code
  MESSAGE "Row Updated."
  SLEEP 1
  MESSAGE ""
END FUNCTION
FUNCTION delete_klist()
  DELETE FROM keylist WHERE kcode= T_keylist.kcode
  CLEAR FORM
  MESSAGE "Row Deleted."
  SLEEP 1
  MESSAGE ""
END FUNCTION
FUNCTION query_klist()
  clear form
  let int_flag = 0
  construct query1 on kcode, kword from keylist.*
  if int_flag <> 0 then return end if
  let select1 = "select * from keylist where ", query1 clipped
  prepare select_key from select1
  let select2 = "select count(*) from keylist where ", query1 clipped
  prepare kl_cnt from select2
  declare kl_curs cursor for kl_cnt
  foreach kl_curs into cnt
    end foreach
  declare k_curs SCROLL CURSOR FOR select_key
  let chosen = FALSE
  OPEN k_curs
  call view_klist()
  CLOSE k_curs
END FUNCTION
FUNCTION view_klist()
  FETCH FIRST k_curs into T_keylist.*
  IF status = NOTFOUND THEN
    MESSAGE "No Keyword Found"
    SLEEP 1
    MESSAGE ""
  ELSE
    display " ", cnt, " rows found" at 9,3 attribute(reverse)
    CALL dispkey()
    CALL view_klist()
  END IF
  let tmp_cnt = 1
  display "" at 9,3
  MENU "BROWSE"
  COMMAND "Next"
    "View the next Keyword in the list." HELP 170
```

```

    FETCH NEXT k_curs INTO T_keylist.*
    let tmp_cnt = tmp_cnt + 1
    IF status = NOTFOUND THEN
        MESSAGE "No more Keywords in this direction."
        SLEEP 1
        let tmp_cnt = cnt
        MESSAGE ""
        FETCH FIRST k_curs INTO T_keylist.*
        END IF
    display " ", tmp_cnt, " of ", cnt, " rows" at 9,3
    attribute(reverse)
    call dispkey()

COMMAND "Previous"
    "View the Previous Keyword in the list." HELP 170
    FETCH PREVIOUS k_curs INTO T_keylist.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
        MESSAGE "No more Keywords in this direction."
        SLEEP 1
        MESSAGE ""
        let tmp_cnt = 1
        FETCH FIRST k_curs INTO T_keylist.*
        END IF
    display " ", tmp_cnt, " of ", cnt, " rows" at 9,3
    attribute(reverse)
    call dispkey()

COMMAND "First"
    "View the first Keyword in the list." HELP 170
    FETCH FIRST k_curs INTO T_keylist.*
    let tmp_cnt = 1
    display " ", tmp_cnt, " of ", cnt, " rows" at 9,3
    attribute(reverse)
    call dispkey()

COMMAND "Last"
    "View the Last Keyword in the list." HELP 170
    message "Searching for last record...."
    FETCH LAST k_curs INTO T_keylist.*
    let tmp_cnt = cnt
    message ""
    display " ", tmp_cnt, " of ", cnt, " rows" at 9,3
    attribute(reverse)
    message ""
    call dispkey()

COMMAND "Update"
    "Update Keyword in Keyword Vocabulary" HELP 171
    call update_klist()

COMMAND "Delete"
    "Delete Keyword from Keyword Vocabulary" HELP 910
    prompt "Are you sure you want to delete this Keyword (y/n)? "
    for answer
    IF answer = "y"
        then
            call delete_klist()
        else
            next option "Next"

```


Toxin Knowledge System Source Code

```
END IF
COMMAND "Exit" "Leave this menu" HELP 2
EXIT MENU
END MENU
END FUNCTION
FUNCTION dispkey()
display by name T_keylist.*
END FUNCTION
```

#tksvoc2.4gl

```
{
TITLE: tksvoc2.4gl
Copyright, Harold L. Trammel, 1987-1988
University of Illinois, CVM, IAPIC
Funded by US Army Contract DAMD-17-C-7114
Purpose: provide basic clinical finding vocabulary management menu,
site vocabulary, morphology vocabulary
Contains the following functions:
s_list()
add_site()
update_site()
delete_site()
find_site()
view_site()
add_morph()
find_morph()
morph_find()
view_morph()
update_morph(tmp_morphnum)
delete_morph(tmp_morphnum)
see_morph(tmp_morphnum)
morphsyn_find()
view_morphsyn()
see_morphsyn(tmp_morphcode)
}
```

DATABASE tkstest

GLOBALS "tksglob.4gl"

#####

FUNCTION s_list()

menu "SIGN-VOCABULARY"

COMMAND "Site"

"Site information" HELP 913

menu "SITE-VOCABULARY"

COMMAND "Add" "Add Site Information"

call add_site()

COMMAND "Find" "Find Site Information"

call find_site()

COMMAND "Exit" "Exit menu"

exit menu

end menu

COMMAND "Morphology"

"Access Morphology Vocabulary" HELP 911

menu "MORPHOLOGY-VOCABULARY"

```

COMMAND "Add" "Add Morphology Information"
  call add_morph()
COMMAND "Find" "Find Morphology Information"
  call find_morph()
COMMAND "Exit" "Exit menu"
  exit menu
end menu
COMMAND "Lab-Test"
  "Access Laboratory Test Vocabulary" HELP 912
  menu "LAB-TEST-VOCABULARY"
    COMMAND "Add" "Add Lab-Test Information"
      call add_lab()
    COMMAND "Find" "Find Lab-Test Information"
      call find_lab()
    COMMAND "Exit" "Exit menu"
      exit menu
  end menu
COMMAND "Disease"
  "Access Disease Vocabulary" HELP 914
  menu "DISEASE-VOCABULARY"
    COMMAND "Add" "Add Disease Information"
      call add_sign()
    COMMAND "Find" "Find Disease Information"
      call find_sign()
    COMMAND "Exit" "Exit menu"
      exit menu
  end menu
COMMAND "Exit"
  "Exit from Sign Vocabulary Modification" HELP 2
  exit menu
END menu
END FUNCTION
#####
FUNCTION add_site()
  call sitewinopen()
  let sw = 0
  INPUT by name T_tkssite.*
  ON KEY (INTERRUPT)
    let sw = 1
  EXIT INPUT
END INPUT
IF sw = 1 then RETURN END IF
insert into tkssite values (T_tkssite.*)
MESSAGE "Row Added"
sleep 1
MESSAGE ""
call sitewinclose()
END FUNCTION
#####
FUNCTION update_site()
  let sw = 0
  INPUT BY NAME T_tkssite.* WITHOUT DEFAULTS
  ON KEY (INTERRUPT)
    let sw = 1
  EXIT INPUT
END INPUT

```

Toxin Knowledge System Source Code

```
IF sw = 1 then RETURN END IF
UPDATE tkssite
  SET tkssite.* = T_tkssite.*
  where tkssite.sitecode= T_tkssite.sitecode

MESSAGE "Row Updated."
SLEEP 3
MESSAGE ""
END FUNCTION
#####
FUNCTION delete_site()
DELETE FROM tkssite WHERE sitecode= T_tkssite.sitecode
MESSAGE "Row Deleted."
SLEEP 3
MESSAGE ""
END FUNCTION
#####
FUNCTION flnd_site()
define
  query1 char(300),
  select1 char(300),
  answer char(1),
  found smallint
call sitewinopen()
message " Enter search criteria and hit ESC "
let int_flag = 0
construct query1
on
  sitecode,
  systemcode, systemname,
  organcode, organnname,
  locatocode, locatename,
  snotopnum
from tkssite.*
if int_flag <> 0 then return end if
let select1 = "select * from tkssite where ", query1 clipped
prepare select_1 from select1
let select2 = "select count(*) from tkssite where ",query1 clipped
prepare sn_cnt from select2
display " Searching . . . " at 17,2 attribute(reverse)
declare sn_curs cursor for sn_cnt
foreach sn_curs into cnt
  end foreach
declare q_curs SCROLL CURSOR FOR select_1
let chosen = FALSE
OPEN q_curs
CALL view_site()
CLOSE q_curs
call sitewinclose()
END FUNCTION
#####
FUNCTION view_site()
let tmp_cnt = 1
FETCH FIRST q_curs into T_tkssite.*
IF status = NOTFOUND
  THEN
    MESSAGE "No Site Found"
```

```

SLEEP 3
MESSAGE ""
ELSE
  display "" at 17,2
  display " ", cnt, " rows found" at 17,2 attribute(reverse)
  DISPLAY BY NAME T_tkssite.*
END IF
MENU "BROWSE"
  COMMAND "Next"
    "View the next site in the list." HELP 170
    FETCH NEXT q_curs INTO T_tkssite.*
    let tmp_cnt = tmp_cnt + 1
    IF status = NOTFOUND THEN
      MESSAGE "No more sites in this direction."
      SLEEP 3
      let tmp_cnt = cnt
      MESSAGE ""
      FETCH LAST q_curs INTO T_tkssite.*
    END IF
    display "" at 17,2
    display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
    attribute(reverse)
    DISPLAY BY NAME T_tkssite.*
  COMMAND "Previous"
    "View the Previous site in the list." HELP 170
    FETCH PREVIOUS q_curs INTO T_tkssite.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
      MESSAGE "No more sites in this direction."
      SLEEP 3
      MESSAGE ""
      let tmp_cnt = 1
      FETCH FIRST q_curs INTO T_tkssite.*
    END IF
    display "" at 17,2
    display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
    attribute(reverse)
    DISPLAY BY NAME T_tkssite.*
  COMMAND "First"
    "View the first site in the list." HELP 170
    FETCH FIRST q_curs INTO T_tkssite.*
    let tmp_cnt = 1
    display "" at 17,2
    display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
    attribute(reverse)
    DISPLAY BY NAME T_tkssite.*
  COMMAND "Last"
    "View the Last site in the list." HELP 170
    FETCH LAST q_curs INTO T_tkssite.*
    let tmp_cnt = cnt
    message ""
    display "" at 17,2
    display " ", tmp_cnt, " of ", cnt, " rows" at 17,2
    attribute(reverse)
    DISPLAY BY NAME T_tkssite.*
  COMMAND "Update"
    "Update site in Site Vocabulary" HELP 171

```

```

    call update_site()
COMMAND "Delete"
    "Delete site from Site Vocabulary" HELP 915
    prompt "Are you sure you want to delete this site (y/n)? "
    for answer
    IF answer = "y" then
        call delete_site()
    END IF
COMMAND "Exit"
    "Leave this menu" HELP 2
    EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION add_morph()
    call morphwinopen()
    let sw = 0
    options input wrap
    input by name T_morphlst.*
    on key (interrupt)
        let sw = 1
        exit input
    after field morphnum
        display "Checking for duplicates ..." at 20,3
        select count(*) into x from morphlst
            where morphnum = T_morphlst.morphnum
        if x > 0
            then
                error beep, "Value already used"
                call see_morphsyn(T_morphlst.morphnum)
                next field morphnum
            end if
    after field morphterm
        display "Checking for duplicates ..." at 20,3
        select count(*) into x from morphlst
            where morphterm = T_morphlst.morphterm
        if x > 0
            then
                error beep, "Value already used"
                call see_morphsyn(T_morphlst.morphnum)
                next field morphterm
            end if
    end input
    if sw = 1 then return end if
    insert into morphlst values(T_morphlst.*)
    insert into morphsynlst values(T_morphlst.morphnum,T_morphlst.morphterm)
    call see_morphsyn(T_morphlst.morphnum)
    input array msyn_array without defaults from holder.*
    on key (interrupt)
        let sw = 1
        exit input
    display "Hit ESC to continue" at 20,3

    before field morphcode
        let curr_arr = arr_curr()
        let msyn_array[curr_arr].morphcode = T_morphlst.morphnum
        next field morphsyn

```

```

    end input
    if sw = 1 then return end if
    delete from morphsynlst where morphcode = T_morphlst.morphnum
    for counter = 1 to arr_count()
        insert into morphsynlst values(msyn_array[counter].*)
    end for
END FUNCTION
#####
FUNCTION find_morph()
    call morphwinopen()
    menu "FIND_MORPHOLOGY_VOCABULARY"
        COMMAND "Preferred_Term"
            call morph_find()
        COMMAND "Synonyms"
            call morphsyn_find()
        COMMAND "Exit"
            exit menu
    end menu
    call morphwinclose()
END FUNCTION

#####
FUNCTION morph_find()
    let int_flag=0
    construct query1
        on
            morphnum, morphterm, morphdef, morphsnocde, morphsnotrm
        from
            morphnum, morphterm, morphdef, morphsnocde, morphsnotrm
    if int_flag <> 0 then return end if
    let select1 = "Select * from morphlst where ", query1 clipped
    prepare find_morph from select1
    let select2 = "select count(*) from morphlst where ", query1 clipped
    prepare cnt_morph from select2
    display " Searching ... " at 20,3
    declare cnt_mrph cursor for cnt_morph
    foreach cnt_mrph into cnt
        end foreach
    close cnt_mrph
    declare m_curs scroll cursor for find_morph
    open m_curs
    call view_morph()
    close m_curs
END FUNCTION
#####
FUNCTION view_morph()
    let tmp_cnt = 1
    FETCH FIRST m_curs into T_morphlst.*
    IF status = NOTFOUND
        THEN
            MESSAGE "No Morphology Found"
            SLEEP 3
            MESSAGE ""
        ELSE
            display "" at 20,3
            display " ", cnt, " rows found" at 20,3 attribute(reverse)
            DISPLAY BY NAME T_morphlst.*

```

Toxin Knowledge System Source Code

```
call see_morphsyn(T_morphlst.morphnum)
END IF
MENU "BROWSE"
COMMAND "Next"
  "View the next term in the list." HELP 170
  FETCH NEXT m_curs INTO T_morphlst.*
  let tmp_cnt = tmp_cnt + 1
  IF status = NOTFOUND THEN
    MESSAGE "No more term in this direction."
    SLEEP 3
    let tmp_cnt = cnt
    MESSAGE ""
    FETCH LAST m_curs INTO T_morphlst.*
  END IF
  display "" at 20,3
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
  attribute(reverse)
  DISPLAY BY NAME T_morphlst.*
  call see_morphsyn(T_morphlst.morphnum)
COMMAND "Previous"
  "View the Previous term in the list." HELP 170
  FETCH PREVIOUS m_curs INTO T_morphlst.*
  let tmp_cnt = tmp_cnt - 1
  IF status = NOTFOUND THEN
    MESSAGE "No more terms in this direction."
    SLEEP 3
    MESSAGE ""
    let tmp_cnt = 1
    FETCH FIRST m_curs INTO T_morphlst.*
  END IF
  display "" at 20,3
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
  attribute(reverse)
  DISPLAY BY NAME T_morphlst.*
  call see_morphsyn(T_morphlst.morphnum)
COMMAND "First"
  "View the first term in the list." HELP 170
  FETCH FIRST m_curs INTO T_morphlst.*
  let tmp_cnt = 1
  display "" at 20,3
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
  attribute(reverse)
  DISPLAY BY NAME T_morphlst.*
  call see_morphsyn(T_morphlst.morphnum)
COMMAND "Last"
  "View the Last term in the list." HELP 170
  FETCH LAST m_curs INTO T_morphlst.*
  let tmp_cnt = cnt
  message ""
  display "" at 20,3
  display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
  attribute(reverse)
  DISPLAY BY NAME T_morphlst.*
  call see_morphsyn(T_morphlst.morphnum)
COMMAND "Update"
  "Update term in Morphology Vocabulary" HELP 171
  call update_morph(T_morphlst.morphnum)
```

```

COMMAND "Delete"
  "Delete term from Morphology Vocabulary" HELP 915
  prompt "Are you sure you want to delete this term (y/n)? "
  for answer
    IF answer = "y" then
      call delete_morph(T_morphlst.morphnum)
    END IF
  COMMAND "Exit"
    "Leave this menu" HELP 2
  EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION update_morph(tmp_morphnum)
  define
    tmp_morphnum like morphlst.morphnum,
    tmp_morphterm like morphlst.morphterm
  let tmp_morphterm = T_morphlst.morphterm
  options input wrap
  input by name T_morphlst.* without defaults
  on key (interrupt)
    let sw = 1
    exit input
  after field morphnum
    if T_morphlst.morphnum <> tmp_morphnum
      then
        select count(*) into x from morphlst
          where morphnum = T_morphlst.morphnum
        if x > 0
          then
            error beep, "Value already used"
            call see_morphsyn(T_morphlst.morphnum)
            next field morphnum
          end if
        end if
      after field morphterm
        if T_morphlst.morphterm <> tmp_morphterm
          then
            select count(*) into x from morphlst
              where morphterm = T_morphlst.morphterm
            if x > 0
              then
                error beep, "Value already used"
                call see_morphsyn(T_morphlst.morphterm)
                next field morphterm
              end if
            end if
          end input
        if sw = 1 then return end if
        update morphlst set morphlst.* = T_morphlst.*
        {
          THERE MAY NEED TO BE A MECHANISM FOR UPDATING LINKED SYNONYMS
        }
      END FUNCTION
#####
FUNCTION delete_morph(tmp_morphnum)
  define

```


Toxin Knowledge System Source Code

```
tmp_morphnum like morphlst.morphnum
call alrt260open()
prompt "Do you really want to delete this term? (y/n) "
for answer
if upshift(answer) = "N"
then
message "Row not deleted"
sleep 1
message ""
return
else
select count(*) into x from morphsynlst
where morphcode = tmp_morphnum
if x > 1
then
DELETE FROM morphlst WHERE morphnum= tmp_morphnum
MESSAGE "Row Deleted."
SLEEP 1
MESSAGE ""
else
prompt "There are associated synonyms. Delete them also? (y/n) "
for answer
if upshift(answer) = "Y"
then
delete from morphsynlst
where morphcode = tmp_morphnum
else
return
end if
end if
end if
call alrt260close()
END FUNCTION
#####
FUNCTION see_morph(tmp_morphnum)
define
tmp_morphnum like morphlst.morphnum
select * into T_morphlst.* from morphlst
where morphnum = tmp_morphnum
display by name T_morphlst.*
END FUNCTION
#####
FUNCTION morphsyn_find()
let int_flag=0
construct query1 on morphcode, morphsyn from holder.*
if int_flag <> 0 then return end if
let select1 = "Select * from morphsynlst where ", query1 clipped
prepare find_morphsyn from select1
let select2 = "select count(*) from morphsynlst where ", query1 clipped
prepare cnt_morphsyn from select2
display " Searching .... " at 20,3
declare cnt_mrphsyn cursor for cnt_morphsyn
foreach cnt_mrphsyn into cnt
end foreach
close cnt_mrphsyn
declare msyn_curs scroll cursor for find_morphsyn
open msyn_curs
```

```

call view_morphsyn()
close msyn_curs
END FUNCTION
#####
FUNCTION view_morphsyn()
let tmp_cnt = 1
FETCH FIRST msyn_curs INTO T_morphsynlst.*
IF status = NOTFOUND
THEN
MESSAGE "No Morphology Found"
SLEEP 3
MESSAGE ""
ELSE
display "" at 20,3
display " ", cnt, " rows found" at 20,3 attribute(reverse)
DISPLAY BY NAME T_morphsynlst.*
call see_morph(T_morphsynlst.morphcode)
END IF
MENU "BROWSE"
COMMAND "Next"
"View the next term in the list." HELP 170
FETCH NEXT msyn_curs INTO T_morphsynlst.*
let tmp_cnt = tmp_cnt + 1
IF status = NOTFOUND THEN
MESSAGE "No more terms in this direction."
SLEEP 3
let tmp_cnt = cnt
MESSAGE ""
FETCH LAST msyn_curs INTO T_morphsynlst.*
END IF
display "" at 20,3
display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
attribute(reverse)
DISPLAY BY NAME T_morphsynlst.*
call see_morph(T_morphsynlst.morphcode)
COMMAND "Previous"
"View the Previous term in the list." HELP 170
FETCH PREVIOUS msyn_curs INTO T_morphsynlst.*
let tmp_cnt = tmp_cnt - 1
IF status = NOTFOUND THEN
MESSAGE "No more terms in this direction."
SLEEP 3
MESSAGE ""
let tmp_cnt = 1
FETCH FIRST msyn_curs INTO T_morphsynlst.*
END IF
display "" at 20,3
display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
attribute(reverse)
DISPLAY BY NAME T_morphsynlst.*
call see_morph(T_morphsynlst.morphcode)
COMMAND "First"
"View the first term in the list." HELP 170
FETCH FIRST msyn_curs INTO T_morphsynlst.*
let tmp_cnt = 1
display "" at 20,3
display " ", tmp_cnt, " of ", cnt, " rows" at 20,3

```

```

        attribute(reverse)
        DISPLAY BY NAME T_morphsynlst.*
        call see_morph(T_morphsynlst.morphcode)
    COMMAND "Last"
        "View the Last term in the list." HELP 170
        FETCH LAST msyn_curs INTO T_morphsynlst.*
        let tmp_cnt = cnt
        message ""
        display "" at 20,3
        display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
        attribute(reverse)
        DISPLAY BY NAME T_morphsynlst.*
        call see_morph(T_morphsynlst.morphcode)
    COMMAND "Update"
        "Update term in Morphology Vocabulary" HELP 171
        #call update_morphsyn(T_morphsynlst.morphcode)
    COMMAND "Exit"
        "Leave this menu" HELP 2
    EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION see_morphsyn(tmp_morphcode)
    define tmp_morphcode like morphsynlst.morphcode
    display " Hit ESC to leave array" at 20,3 attribute(reverse)
    declare morph_see cursor for
        select * from morphsynlst
            where morphcode = tmp_morphcode
            order by morphsyn
    let counter = 1
    foreach morph_see into msyn_array[counter].*
        let counter = counter + 1
        if counter > 50
            then exit foreach
        end if
    end foreach
    call set_count(counter - 1)
    display array msyn_array to holder.*
        on key(interrupt)
            exit display
    end display
    close morph_see
END FUNCTION

```

#tksvoc3.4gl

{

TITLE: tksvoc3.4gl

Copyright, Harold L. Trammel, 1987-1988

University of Illinois, CVM, IAPIC

Funded by US Army Contract DAMD-17-C-7114

Contains the following functions:

```

add_lab()
find_lab()
lab_find()
view_lab()
update_lab(tmp_labnum)
delete_lab(tmp_labnum)
see_lab(tmp_labnum)
labsyn_find()
view_labsyn()
see_labsyn(tmp_labcode)
add_sign()
find_sign()
sign_find()
view_sign()
update_sign(tmp_signnum)
delete_sign(tmp_signnum)
see_sign(tmp_signnum)
signsyn_find()
view_signsyn()
see_signsyn(tmp_signcode)

```

}

DATABASE tkstest

GLOBALS "tksglob.4gl"

#####

FUNCTION add_lab()

```

call labwinopen()
let sw = 0
options input wrap
input by name T_lablst.*
  on key (interrupt)
    let sw = 1
    exit input
  after field labnum
    display "Checking for duplicates ..." at 20,3
    select count(*) into x from lablst
      where labnum = T_lablst.labnum
    if x > 0
      then
        error beep, "Value already used"
        call see_labsyn(T_lablst.labnum)
        next field labnum
      end if
  after field labterm
    display "Checking for duplicates ..." at 20,3
    select count(*) into x from lablst
      where labterm = T_lablst.labterm
    if x > 0
      then

```

Toxin Knowledge System Source Code'

```
        error beep, "Value already used"
        call see_labsyn(T_lablst.labnum)
        next field labterm
    end if
end input
if sw = 1 then return end if
insert into lablst values(T_lablst.*)
insert into labsynlst
    values(T_lablst.labnum,T_lablst.labsys,T_lablst.labterm)
call see_labsyn(T_lablst.labnum)
input array lsyn_array without defaults from holder.*
    on key (interrupt)
        let sw =1
        exit input
    display "Hit ESC to continue" at 20,3
    before field labcode
        let curr_arr = arr_curr()
        let lsyn_array[curr_arr].labcode = T_lablst.labnum
        next field labsyn
    end input
if sw = 1 then return end if
delete from labsynlst where labcode = T_lablst.labnum
for counter = 1 to arr_count()
    insert into labsynlst values(lsyn_array[counter].*)
end for
END FUNCTION
#####
FUNCTION flnd_lab()
    call labwinopen()
    menu "FIND_LAB_VOCABULARY"
        COMMAND "Preferred_Term"
            call lab_find()
        COMMAND "Synonyms"
            call labsyn_find()
        COMMAND "Exit"
            exit menu
    end menu
call labwinclose()
END FUNCTION

#####
FUNCTION lab_flnd()
    clear form
    let int_flag=0
    construct query1
        on
            labnum, labterm, labsyn, labdef, labsnocde, labsnotrm
        from
            labnum, labterm, labsyn, labdef, labsnocde, labsnotrm
    if int_flag <> 0 then return end if
    let select1 = "Select * from lablst where ", query1 clipped
    prepare find_lab from select1
    let select2 = "select count(*) from lablst where ", query1 clipped
    prepare cnt_lab from select2
    display " Searching .... " at 20,3
    declare cnt_labs cursor for cnt_lab
    foreach cnt_labs into cnt
```

```

    end foreach
  close cnt_labs
  declare l_curs scroll cursor for find_lab
  open l_curs
  call view_lab()
  close l_curs
  END FUNCTION
#####
FUNCTION view_lab()
  let tmp_cnt = 1
  FETCH FIRST l_curs into T_lablst.*
  IF status = NOTFOUND
    THEN
      MESSAGE "No Lab Test Found"
      SLEEP 3
      MESSAGE ""
    ELSE
      display "" at 20,3
      display " ", cnt, " rows found" at 20,3 attribute(reverse)
      DISPLAY BY NAME T_lablst.*
      call see_labsyn(T_lablst.labnum)
    END IF
  MENU "BROWSE"
  COMMAND "Next"
    "View the next term in the list." HELP 170
    FETCH NEXT l_curs INTO T_lablst.*
    let tmp_cnt = tmp_cnt + 1
    IF status = NOTFOUND THEN
      MESSAGE "No more terms in this direction."
      SLEEP 3
      let tmp_cnt = cnt
      MESSAGE ""
      FETCH LAST l_curs INTO T_lablst.*
    END IF
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
    attribute(reverse)
    DISPLAY BY NAME T_lablst.*
    call see_labsyn(T_lablst.labnum)
  COMMAND "Previous"
    "View the Previous term in the list." HELP 170
    FETCH PREVIOUS l_curs INTO T_lablst.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
      MESSAGE "No more terms in this direction."
      SLEEP 3
      MESSAGE ""
      let tmp_cnt = 1
      FETCH FIRST l_curs INTO T_lablst.*
    END IF
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
    attribute(reverse)
    DISPLAY BY NAME T_lablst.*
    call see_labsyn(T_lablst.labnum)
  COMMAND "First"
    "View the first term in the list." HELP 170

```

Toxin Knowledge System Source Code

```
    FETCH FIRST l_curs INTO T_lablst.*
    let tmp_cnt = 1
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
        attribute(reverse)
    DISPLAY BY NAME T_lablst.*
    call see_labsyn(T_lablst.labnum)
COMMAND "Last"
    "View the Last term in the list." HELP 170
    FETCH LAST l_curs INTO T_lablst.*
    let tmp_cnt = cnt
    message ""
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
        attribute(reverse)
    DISPLAY BY NAME T_lablst.*
    call see_labsyn(T_lablst.labnum)
COMMAND "Update"
    "Update term in Lab Test Vocabulary" HELP 171
    call update_lab(T_lablst.labnum)
COMMAND "Delete"
    "Delete term from Lab Test Vocabulary" HELP 915
    prompt "Are you sure you want to delete this term (y/n)? "
        for answer
    IF answer = "y" then
        call delete_lab(T_lablst.labnum)
    END IF
COMMAND "Exit"
    "Leave this menu" HELP 2
    EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION update_lab(tmp_labnum)
    define
        tmp_labnum like lablst.labnum,
        tmp_labterm like lablst.labterm
    let tmp_labterm = T_lablst.labterm
    options input wrap
    input by name T_lablst.* without defaults
        on key (interrupt)
            let sw = 1
            exit input
    after field labnum
        if T_lablst.labnum <> tmp_labnum
            then
                select count(*) into x from lablst
                    where labnum = T_lablst.labnum
                if x > 0
                    then
                        error beep, "Value already used"
                        call see_labsyn(T_lablst.labnum)
                        next field labnum
                    end if
            end if
    after field labterm
        if T_lablst.labterm <> tmp_labterm
```

```

        then
            select count(*) into x from lablst
            where labterm = T_lablst.labterm
            if x > 0
                then
                    error beep, "Value already used"
                    call see_labsyn(T_lablst.labterm)
                    next field labterm
                end if
            end if
        end input
    if sw = 1 then return end if
    update lablst set lablst.* = T_lablst.*
    {
        THERE MAY NEED TO BE A MECHANISM FOR UPDATING LINKED SYNONYMS
    }
    END FUNCTION
#####
FUNCTION delete_lab(tmp_labnum)
    define
        tmp_labnum like lablst.labnum
    call alrt260open()
    prompt "Do you really want to delete this term? (y/n) "
    for answer
    if upshift(answer) = "N"
        then
            message "Row not deleted"
            sleep 1
            message ""
            return
        else
            select count(*) into x from labsynlst
            where labcode = tmp_labnum
            if x > 1
                then
                    DELETE FROM lablst WHERE labnum= tmp_labnum
                    MESSAGE "Row Deleted."
                    SLEEP 1
                    MESSAGE ""
                else
                    prompt "There are associated synonyms. Delete them also? (y/n) "
                    for answer
                    if upshift(answer) = "Y"
                        then
                            delete from labsynlst
                            where labcode = tmp_labnum
                        else
                            return
                        end if
                    end if
                end if
            end if
        end if
    call alrt260close()
    END FUNCTION
#####
FUNCTION see_lab(tmp_labnum)
    define tmp_labnum like lablst.labnum
    select * into T_lablst.* from lablst

```


Toxic Knowledge System Source Code

```
        where labnum = tmp_labnum
        display by name T_lablst.*
    END FUNCTION
#####
FUNCTION labsyn_find()
    clear form
    let int_flag=0
    construct query1 on labcode, labsyn, labsynsys from holder.*,labsynsys
    if int_flag <> 0 then return end if
    let select1 = "Select * from labsynlst where ", query1 clipped
    prepare find_labsyn from select1
    let select2 = "select count(*) from labsynlst where ", query1 clipped
    prepare cnt_labsyn from select2
    display " Searching .... " at 20,3
    declare cnt_labssyn cursor for cnt_labsyn
    foreach cnt_labssyn into cnt
        end foreach
    close cnt_labssyn
    declare lsyn_curs scroll cursor for find_labsyn
    open lsyn_curs
    call view_labsyn()
    close lsyn_curs
END FUNCTION
#####
FUNCTION view_labsyn()
    let tmp_cnt = 1
    FETCH FIRST lsyn_curs into T_labsynlst.*
    IF status = NOTFOUND
        THEN
            MESSAGE "No Lab Test Found"
            SLEEP 3
            MESSAGE ""
        ELSE
            display "" at 20,3
            display " ", cnt, " rows found" at 20,3 attribute(reverse)
            DISPLAY BY NAME T_labsynlst.*
            call see_lab(T_labsynlst.labcode)
        END IF
    MENU "BROWSE"
    COMMAND "Next"
        "View the next term in the list." HELP 170
        FETCH NEXT lsyn_curs INTO T_labsynlst.*
        let tmp_cnt = tmp_cnt + 1
        IF status = NOTFOUND THEN
            MESSAGE "No more terms in this direction."
            SLEEP 3
            let tmp_cnt = cnt
            MESSAGE ""
            FETCH LAST lsyn_curs INTO T_labsynlst.*
            END IF
        display "" at 20,3
        display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
        attribute(reverse)
        DISPLAY BY NAME T_labsynlst.*
        call see_lab(T_labsynlst.labcode)
    COMMAND "Previous"
        "View the Previous term in the list." HELP 170
```

```

    FETCH PREVIOUS lsyn_curs INTO T_labsynlst.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
        MESSAGE "No more terms in this direction."
        SLEEP 3
        MESSAGE ""
        let tmp_cnt = 1
        FETCH FIRST lsyn_curs INTO T_labsynlst.*
    END IF
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
    attribute(reverse)
    DISPLAY BY NAME T_labsynlst.*
    call see_lab(T_labsynlst.labcode)
COMMAND "First"
    "View the first term in the list." HELP 170
    FETCH FIRST lsyn_curs INTO T_labsynlst.*
    let tmp_cnt = 1
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
    attribute(reverse)
    DISPLAY BY NAME T_labsynlst.*
    call see_lab(T_labsynlst.labcode)
COMMAND "Last"
    "View the Last term in the list." HELP 170
    FETCH LAST lsyn_curs INTO T_labsynlst.*
    let tmp_cnt = cnt
    message ""
    display "" at 20,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 20,3
    attribute(reverse)
    DISPLAY BY NAME T_labsynlst.*
    call see_lab(T_labsynlst.labcode)
COMMAND "Update"
    "Update term in Lab Test Vocabulary" HELP 171
    #call update_labsyn(T_labsynlst.labcode)
COMMAND "Exit"
    "Leave this menu" HELP 2
    EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION see_labsyn(tmp_labcode)
    define
        tmp_labcode like labsynlst.labcode,
        tmp_sys char(1)
    display " Hit ESC to leave array" at 20,3 attribute(reverse)
    declare lab_see cursor for
        select labcode, labsyn, labsynsys from labsynlst
        where labcode = tmp_labcode
        order by labsyn
    let counter = 1
    foreach lab_see into lsyn_array[counter].*, tmp_sys
        let counter = counter + 1
        if counter > 50
            then exit foreach
        end if

```

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```
end foreach
call set_count(counter -1)
display tmp_sys to labsynsys
display array lsyn_array to holder.*
on key(interrupt)
exit display
end display
close lab_see
END FUNCTION
#####
FUNCTION add_sign()
define
tmp_value char(1)
call signwinopen()
let sw = 0
options input wrap
input by name T_signlst.*
on key (interrupt)
let sw =1
exit input
after field signnum
display "Checking for duplicates ..." at 20,3
select count(*) into x from signlst
where signnum = T_signlst.signnum
if x > 0
then
error beep, "Value already used"
call see_signsyn(T_signlst.signnum)
next field signnum
end if
after field signterm
display "Checking for duplicates ..." at 20,3
select count(*) into x from signlst
where sign = T_signlst.sign
if x > 0
then
error beep, "Value already used"
call see_signsyn(T_signlst.signnum)
next field sign
end if
before field systemcode
call system_choice() returning tmp_value
call system_trans(tmp_value)
returning T_signlst.systemcode, T_signlst.systemname
if chosen = 0
then
display by name T_signlst.systemcode, T_signlst.systemname
next field signdef
else next field systemcode
end if
end input
if sw = 1 then return end if
insert into signlst values(T_signlst.*)
insert into signsynlst values(T_signlst.signnum,T_signlst.sign)
call see_signsyn(T_signlst.signnum)
input array ssyn_array without defaults from holder.*
on key (interrupt)
```

```

        let sw = 1
        exit input
    display "Hit ESC to continue" at 20,3
    before field signcode
        let curr_arr = arr_curr()
        let ssyn_array[curr_arr].signcode = T_signlst.signnum
    next field signsyn
end input
if sw = 1 then return end if
delete from signsynlst where signcode = T_signlst.signnum
for counter = 1 to arr_count()
    insert into signsynlst values(ssyn_array[counter].*)
end for
END FUNCTION
#####
FUNCTION find_sign()
    call signwinopen()
    menu "FIND_MORPHOLOGY_VOCABULARY"
        COMMAND "Preferred_Term"
            call sign_find()
        COMMAND "Synonyms"
            call signsyn_find()
        COMMAND "Exit"
    exit menu
end menu
call signwinclose()
END FUNCTION

#####
FUNCTION sign_find()
    let int_flag=0
    construct query1
        or
            signnum, sign, systemcode, systemname, signdef, snocode, snoterm
        from
            signnum, sign, systemcode, systemname, signdef, snocode, snoterm
    if int_flag <> 0 then return end if
    let select1 = "Select * from signlst where ", query1 clipped
    prepare find_sign from select1
    let select2 = "select count(*) from signlst where ", query1 clipped
    prepare cnt_sign from select2
    display " Searching .... " at 19,3
    declare cnt_sgn cursor for cnt_sign
    foreach cnt_sgn into cnt
        end foreach
    close cnt_sgn
    declare s_curs scroll cursor for find_sign
    open s_curs
    call view_sign()
    close s_curs
END FUNCTION
#####
FUNCTION view_sign()
    let tmp_cnt = 1
    FETCH FIRST s_curs into T_signlst.*
    IF status = NOTFOUND
    THEN

```

Toxin Knowledge System Source Code

```
MESSAGE "No Sign/Disease Found"
SLEEP 3
MESSAGE ""
ELSE
  display "" at 19,3
  display " ", cnt, " rows found" at 19,3 attribute(reverse)
  DISPLAY BY NAME T_signlst.*
  call see_signsyn(T_signlst.signnum)
END IF
MENU "BROWSE"
  COMMAND "Next"
    "View the next term in the list." HELP 170
    FETCH NEXT s_curs INTO T_signlst.*
    let tmp_cnt = tmp_cnt + 1
    IF status = NOTFOUND THEN
      MESSAGE "No more terms in this direction."
      SLEEP 3
      let tmp_cnt = cnt
      MESSAGE ""
      FETCH LAST s_curs INTO T_signlst.*
      END IF
    display "" at 19,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
      attribute(reverse)
    DISPLAY BY NAME T_signlst.*
    call see_signsyn(T_signlst.signnum)
  COMMAND "Previous"
    "View the Previous term in the list." HELP 170
    FETCH PREVIOUS s_curs INTO T_signlst.*
    let tmp_cnt = tmp_cnt - 1
    IF status = NOTFOUND THEN
      MESSAGE "No more terms in this direction."
      SLEEP 3
      MESSAGE ""
      let tmp_cnt = 1
      FETCH FIRST s_curs INTO T_signlst.*
      END IF
    display "" at 19,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
      attribute(reverse)
    DISPLAY BY NAME T_signlst.*
    call see_signsyn(T_signlst.signnum)
  COMMAND "First"
    "View the first term in the list." HELP 170
    FETCH FIRST s_curs INTO T_signlst.*
    let tmp_cnt = 1
    display "" at 19,3
    display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
      attribute(reverse)
    DISPLAY BY NAME T_signlst.*
    call see_signsyn(T_signlst.signnum)
  COMMAND "Last"
    "View the Last term in the list." HELP 170
    FETCH LAST s_curs INTO T_signlst.*
    let tmp_cnt = cnt
    message ""
    display "" at 19,3
```

```

display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
attribute(reverse)
DISPLAY BY NAME T_signlst.*
call see_signsyn(T_signlst.signnum)
COMMAND "Update"
  "Update term in Sign/Disease Vocabulary" HELP 171
  call update_sign(T_signlst.signnum)
COMMAND "Delete"
  "Delete term from Sign/Disease Vocabulary" HELP 915
  prompt "Are you sure you want to delete this term (y/n)? "
  for answer
  IF answer = "y" then
    call delete_sign(T_signlst.signnum)
  END IF
COMMAND "Exit"
  "Leave this menu" HELP 2
EXIT MENU
END MENU
END FUNCTION
#####
FUNCTION update_sign(tmp_signnum)
define
  tmp_signnum like signlst.signnum,
  tmp_sign like signlst.sign,
  tmp_sys like signlst.systemname,
  tmp_value char(1)
let tmp_sign = T_signlst.sign
options input wrap
input by name T_signlst.* without defaults
on key (interrupt)
  let sw = 1
  exit input
after field signnum
  if T_signlst.signnum <> tmp_signnum
  then
    select count(*) into x from signlst
      where signnum = T_signlst.signnum
    if x > 0
    then
      error beep, "Value already used"
      call see_signsyn(T_signlst.signnum)
      next field signnum
    end if
  end if
after field sign
  if T_signlst.sign <> tmp_sign
  then
    select count(*) into x from signlst
      where sign = T_signlst.sign
    if x > 0
    then
      error beep, "Value already used"
      call see_signsyn(T_signlst.sign)
      next field sign
    end if
  end if
after field systemcode

```

Toxin Knowledge System Source Code

```
if T_signlst.systemcode is null
then
    call system_choice() returning tmp_value
    call system_trans(tmp_value)
        returning T_signlst.systemcode, T_signlst.systemname
    if chosen = 0
    then
        display by name T_signlst.systemcode, T_signlst.systemname
        next field signdef
    else next field systemcode
    end if
else
    select systemname from tkssite
    where systemcode = T_signlst.systemcode
    and organcode = "—"
    if status = NOTFOUND
    then error beep, "Not acceptable system code"
    call system_choice() returning tmp_value
    call system_trans(tmp_value)
        returning T_signlst.systemcode, T_signlst.systemname
    if chosen = 0
    then
        display by name T_signlst.systemcode, T_signlst.systemname
        next field signdef
    else next field systemcode
    end if
    end if
end if
end input
if sw = 1 then return end if
update signlst set signlst.* = T_signlst.*
(
THERE MAY NEED TO BE A MECHANISM FOR UPDATING LINKED SYNONYMS
)
END FUNCTION
#####
FUNCTION delete_sign(tmp_signnum)
define
    tmp_signnum like signlst.signnum
call alrt260open()
prompt "Do you really want to delete this term? (y/n) "
for answer
if upshift(answer) = "N"
then
    message "Row not deleted"
    sleep 1
    message ""
    return
else
    select count(*) into x from signsynlst
    where signcode = tmp_signnum
    if x > 1
    then
        DELETE FROM signlst WHERE signnum= tmp_signnum
        MESSAGE "Row Deleted."
        SLEEP 1
        MESSAGE ""
```

```

else
    prompt "There are associated synonyms. Delete them also? (y/n) "
    for answer
    if upshift(answer) = "Y"
    then
        delete from signsynlst
            where signcode = tmp_signnum
    else
        return
    end if
    end if
end if
call alrt260close()
END FUNCTION
#####
FUNCTION see_sign(tmp_signnum)
    define tmp_signnum like signlst.signnum
    select * into T_signlst.* from signlst
        where signnum = tmp_signnum
    display by name T_signlst.*
END FUNCTION
#####
FUNCTION signsyn_fnd()
    let int_flag=0
    construct query1 on signcode, signsyn from holder.*
    if int_flag <> 0 then return end if
    let select1 = "Select * from signsynlst where ", query1 clipped
    prepare find_signsyn from select1
    let select2 = "select count(*) from signsynlst where ", query1 clipped
    prepare cnt_signsyn from select2
    display " Searching .... " at 19,3
    declare cnt_sgnsyn cursor for cnt_signsyn
    foreach cnt_sgnsyn into cnt
        end foreach
    close cnt_sgnsyn
    declare ssyn_curs scroll cursor for find_signsyn
    open ssyn_curs
    call view_signsyn()
    close ssyn_curs
END FUNCTION
#####
FUNCTION view_signsyn()
    let tmp_cnt = 1
    FETCH FIRST ssyn_curs into T_signsynlst.*
    IF status = NOTFOUND
    THEN
        MESSAGE "No Sign/Disease Found"
        SLEEP 3
        MESSAGE ""
    ELSE
        display "" at 19,3
        display " ", cnt, " rows found" at 19,3 attribute(reverse)
        DISPLAY BY NAME T_signsynlst.*
        call see_sign(T_signsynlst.signcode)
    END IF
    MENU "BROWSE"
    COMMAND "Next"

```


Toxin Knowledge System Source Code

```
"View the next term in the list." HELP 170
FETCH NEXT ssyn_curs INTO T_signsynlst.*
let tmp_cnt = tmp_cnt + 1
IF status = NOTFOUND THEN
  MESSAGE "No more terms in this direction."
  SLEEP 3
  let tmp_cnt = cnt
  MESSAGE ""
  FETCH LAST ssyn_curs INTO T_signsynlst.*
END IF
display "" at 19,3
display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
attribute(reverse)
DISPLAY BY NAME T_signsynlst.*
call see_sign(T_signsynlst.signcode)
COMMAND "Previous"
"View the Previous term in the list." HELP 170
FETCH PREVIOUS ssyn_curs INTO T_signsynlst.*
let tmp_cnt = tmp_cnt - 1
IF status = NOTFOUND THEN
  MESSAGE "No more terms in this direction."
  SLEEP 3
  MESSAGE ""
  let tmp_cnt = 1
  FETCH FIRST ssyn_curs INTO T_signsynlst.*
END IF
display "" at 19,3
display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
attribute(reverse)
DISPLAY BY NAME T_signsynlst.*
call see_sign(T_signsynlst.signcode)
COMMAND "First"
"View the first term in the list." HELP 170
FETCH FIRST ssyn_curs INTO T_signsynlst.*
let tmp_cnt = 1
display "" at 19,3
display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
attribute(reverse)
DISPLAY BY NAME T_signsynlst.*
call see_sign(T_signsynlst.signcode)
COMMAND "Last"
"View the Last term in the list." HELP 170
FETCH LAST ssyn_curs INTO T_signsynlst.*
let tmp_cnt = cnt
message ""
display "" at 19,3
display " ", tmp_cnt, " of ", cnt, " rows" at 19,3
attribute(reverse)
DISPLAY BY NAME T_signsynlst.*
call see_sign(T_signsynlst.signcode)
COMMAND "Update"
"Update term in Sign/Disease Vocabulary" HELP 171
#call update_signsyn(T_signsynlst.signcode)
COMMAND "Exit"
"Leave this menu" HELP 2
EXIT MENU
END MENU
```

END FUNCTION

#####

FUNCTION see_signsyn(tmp_signcode)

define

tmp_signcode like signsynlst.signcode

display " Hit ESC to leave array" at 19,3 attribute(reverse)

declare sign_see cursor for

select * from signsynlst

where signcode = tmp_signcode

order by signsyn

let counter = 1

foreach sign_see into ssyn_array[counter].*

let counter = counter + 1

if counter > 50

then exit foreach

end if

end foreach

call set_count(counter - 1)

display array ssyn_array to holder.*

on key(interrupt)

exit display

end display

close sign_see

END FUNCTION

Toxin Knowledge System Source Code

#tkstrans.4gl

```
(
  Title: tkstrans.4gl
  Copyright Harold L. Trammel, 1987-1988
  University of Illinois, CVM, IAPIC
  Funded by US Army Contract DAMD-17-C-7114
  Contains the following functions:
    clear_choice(topRow,bottomRow,leftCol)
    aim_choice(aim)
    aim_trans(aim_hold)
    stype_choice()
    stype_trans(tmp_type)
    vivit_choice()
    vivit_trans(hold_vivit)
    cntlcmp_choice()
    cntlcmp_trans(hold_cntlcmp)
    cmpmeth_choice(cntlcmp)
    cmpmeth_trans(cmpmeth)
    cntlmeth_choice()
    cntlmeth_trans(hold_cntlmeth)
    cntltyp_choice(stycntlmeth)
    cntltyp_trans(cntltyp)
    cntlassgn_choice()
    cntlassgn_trans(cntlassgn)
    rte_choice()
    rte_trans(rte)
    sex_choice()
    sex_trans(sex)
    date_choice()
    date_trans(dte)
    wt_choice()
    form_choice()
    form_trans(formul)
    severe_trans(hold_severe)
    pur_choice()
    pur_trans(tmp_val)
    dose_choice()
    change_choice()
    trans_change(tmp_cng)
    system_choice()
    system_trans(tmp_value)
    labCatChoice()
    labCatTran(tmp_value)
)
```

database tkstest

globals "tksglob.4gl"

FUNCTION clear_choice(topRow,bottomRow,leftCol)

define topRow, bottomRow, leftCol smallint

for x = topRow to bottomRow

display "" at x,leftCol

end for

end function

FUNCTION aim_choice(aim)

```

define aim char(1)
call clear_choice(8,16,50)
let chosen = 1
case
  when aim = "0"
    display " E = Experimental " at 8,50 attribute(reverse)
    display " N = Non-Experiment " at 9,50 attribute(reverse)
    display " I = Info Only " at 10,50 attribute(reverse)
    display " C = Combination " at 11,50 attribute(reverse)
    exit case
  when aim = "E"
    display " E10 = Toxicity " at 8, 50 attribute(reverse)
    display " E20 = Mechanisms " at 9, 50 attribute(reverse)
    display " E30 = Kinetics " at 10, 50 attribute(reverse)
    display " E40 = Treatment " at 11, 50 attribute(reverse)
    display " E50 = Pharmacol " at 12, 50 attribute(reverse)
    display " E60 = Chemistry " at 13, 50 attribute(reverse)
    display " E61 = Analysis " at 14, 50 attribute(reverse)
    display " E62 = Synthesis " at 15, 50 attribute(reverse)
    display " E63 = Purific. " at 16, 50 attribute(reverse)
    exit case
  when aim = "N"
    display " N10 = Case Report " at 8, 50 attribute(reverse)
    display " N20 = Epidemiology " at 9, 50 attribute(reverse)
    exit case
  when aim = "I"
    display " I01 = Review " at 8, 50 attribute(reverse)
    display " I02 = Comment " at 9, 50 attribute(reverse)
    exit case
  when aim = "C"
    display " C01 = Case+Review " at 8, 50 attribute(reverse)
    display " C02 = Case+Experi " at 9, 50 attribute(reverse)
    display " C03 = Exper+Revue " at 10, 50 attribute(reverse)
    exit case
  otherwise
    error beep, "Not an acceptable choice"
    let chosen = 0
    exit case
end case
end function

```

```

#####

```

FUNCTION aim_trans(aim_hold)

```

define
  aim_hold like paperover.papaim,
  aim_class char(20)
let chosen = 1
Case
  when aim_hold = "E10"
    let aim_class = "EXPER-TOXICITY"
    exit case
  when aim_hold = "E20"
    let aim_class = "EXPER-MECHANISMS"
    exit case
  when aim_hold = "E30"
    let aim_class = "EXPER-KINETICS"
    exit case

```

Toxin Knowledge System Source Code

```
when aim_hold = "E40"
  let aim_class = "EXPER-TREAT"
  exit case
when aim_hold = "E50"
  let aim_class = "EXPER-PHARMACOL"
  exit case
when aim_hold = "E60"
  let aim_class = "EXP-CHEM-NOS"
  exit case
when aim_hold = "E61"
  let aim_class = "EXP-CHEM-ANALYT"
  exit case
when aim_hold = "E62"
  let aim_class = "EXP-CHEM-SYNTH"
  exit case
when aim_hold = "E63"
  let aim_class = "EXP-CHEM-PURIF"
  exit case
when aim_hold = "N10"
  let aim_class = "CASE REPORT"
  exit case
when aim_hold = "N20"
  let aim_class = "EPIDEMIOLOGY"
  exit case
when aim_hold = "T10"
  let aim_class = "REVIEW"
  exit case
when aim_hold = "I20"
  let aim_class = "COMMENT"
  exit case
when aim_hold = "C01"
  let aim_class = "CASE-REVIEW"
  exit case
when aim_hold = "C02"
  let aim_class = "CASE-EXPER"
  exit case
when aim_hold = "C03"
  let aim_class = "EXPER-REVUE"
  exit case
when aim_hold = "C04"
  let aim_class = "CASE-EPIDEM"
  exit case
when aim_hold = "C05"
  let aim_class = "EXPR-EPIDEM"
  exit case
otherwise
  error beep, "Not an acceptable choice"
  let aim_class = " "
  let chosen = 0
  exit case
end case
return aim_class
end FUNCTION
#####
FUNCTION stype_choice(tmp_aim)
  define
    tmp_aim like paperover.papaim
```

```

call clear_choice(8,16,50)
case
  when tmp_aim[1] = "N" or tmp_aim = "C04"
    display " A = Survey      " at 8,50 attribute(reverse)
    display " A1 = Prospective " at 9,50 attribute(reverse)
    display " A2 = Retrospective " at 10,50 attribute(reverse)
    display " F = Case Report   " at 15,50 attribute(reverse)
    exit case
  when tmp_aim[1] = "E"
    display " B = Experiment    " at 11,50 attribute(reverse)
    display " C = Therapeutic   " at 12,50 attribute(reverse)
    display " D = Prophylactic  " at 13,50 attribute(reverse)
    display " E = Symptomatic   " at 14,50 attribute(reverse)
    exit case
  when tmp_aim = "C01"
    display " F = Case Report   " at 15,50 attribute(reverse)
    exit case
  when tmp_aim = "C02"
    display " B = Experiment    " at 11,50 attribute(reverse)
    display " C = Therapeutic   " at 12,50 attribute(reverse)
    display " D = Prophylactic  " at 13,50 attribute(reverse)
    display " E = Symptomatic   " at 14,50 attribute(reverse)
    display " F = Case Report   " at 15,50 attribute(reverse)
    exit case
  when tmp_aim = "C03"
    display " B = Experiment    " at 11,50 attribute(reverse)
    display " C = Therapeutic   " at 12,50 attribute(reverse)
    display " D = Prophylactic  " at 13,50 attribute(reverse)
    display " E = Symptomatic   " at 14,50 attribute(reverse)
    exit case
  when tmp_aim = "C05"
    display " A = Survey      " at 8,50 attribute(reverse)
    display " A1 = Prospective " at 9,50 attribute(reverse)
    display " A2 = Retrospective " at 10,50 attribute(reverse)
    display " B = Experiment    " at 11,50 attribute(reverse)
    display " C = Therapeutic   " at 12,50 attribute(reverse)
    display " D = Prophylactic  " at 13,50 attribute(reverse)
    display " E = Symptomatic   " at 14,50 attribute(reverse)
    display " F = Case Report   " at 15,50 attribute(reverse)
    exit case
end case
end function
#####
FUNCTION style_trans(tmp_type)
define
  tmp_type like stdydsgr.stytype,
  hold_type char(20)
let chosen = 1
case
  when tmp_type = "A"
    let hold_type = "SURVEY NOS"
    exit case
  when tmp_type = "A1"
    let hold_type = "SURVEY-PRO"
    exit case
  when tmp_type = "A2"
    let hold_type = "SURVEY-RETRO"

```

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```
    exit case
  when tmp_type = "B"
    let hold_type = "EXPERIMENT"
  exit case
  when tmp_type = "C"
    let hold_type = "THERAPEUTIC"
  exit case
  when tmp_type = "D"
    let hold_type = "PROPHYLACTIC"
  exit case
  when tmp_type = "E"
    let hold_type = "SYMPTOMATIC"
  exit case
  when tmp_type = "F"
    let hold_type = "CASE REPORT"
  exit case
  otherwise
    let hold_type = "NONE"
    let chosen = 1
  exit case
end case
return hold_type
END FUNCTION
#####
FUNCTION vivit_choice()
  call clear_choice(8,16,50)
  display " V = in viVo   " at 8,50 attribute(reverse)
  display " T = in viTro  " at 9,50 attribute(reverse)
  display " I = Info only " at 10,50 attribute(reverse)
end function
#####
FUNCTION vivit_trans(hold_vivit)
  define
    hold_vivit like stdydsgrn.styvivit,
    tmp_vivit char(10)
  let chosen = 1
  Case
    when hold_vivit = "V"
      let tmp_vivit = "IN VIVO"
    exit case
    when hold_vivit = "T"
      let tmp_vivit = "IN VITRO"
    exit case
    when hold_vivit = "I"
      let tmp_vivit = "INFO ONLY"
    exit case
  otherwise
    error beep, "Not an acceptable choice"
    let tmp_vivit = " "
    let chosen = 0
  exit case
  end case
  return tmp_vivit
end function
#####
FUNCTION cntlcmp_choice()
  call clear_choice(8,16,50)
```

```

display " A = Between Groups " at 12, 50 attribute(reverse)
display " B = Within Groups " at 13, 50 attribute(reverse)
display " C = Combination of A & B " at 14, 50 attribute(reverse)
display " U = Unknown " at 15, 50 attribute(reverse)
end function
#####
FUNCTION cntlcmp_trans(hold_cntlcmp)
  define hold_cntlcmp like stdydsgrn.stycntlcmp,
    tmp_cntlcmp char(20)
  let chosen = 1
  case
    when hold_cntlcmp = "A"
      let tmp_cntlcmp = "BETWEEN GROUP"
      exit case
    when hold_cntlcmp = "B"
      let tmp_cntlcmp = "WITHIN GROUP"
      exit case
    when hold_cntlcmp = "C"
      let tmp_cntlcmp = "BETWEEN & WITHIN GRS "
      exit case
    when hold_cntlcmp = "U"
      let tmp_cntlcmp = "UNKNOWN"
      exit case
    otherwise
      error beep, "Not an acceptable choice"
      let tmp_cntlcmp = " "
      let chosen = 0
      exit case
  end case
  return tmp_cntlcmp
end function
#####
FUNCTION cmpmeth_choice(cntlcmp)
  define
    cntlcmp char(1)
  call clear_choice(8,16,50)
  case
    when cntlcmp = "A"
      display " A1= Non-crossover " at 12,50 attribute(reverse)
      display " A2= One-way " at 13,50 attribute(reverse)
      display " A3= Parallel groups " at 14,50 attribute(reverse)
      exit case
    when cntlcmp = "B"
      display " B1= Crossover " at 12,50 attribute(reverse)
      display " B2= Latin Square " at 13,50 attribute(reverse)
      display " B3= Randomized Blocks " at 14,50 attribute(reverse)
      exit case
    when cntlcmp = "C"
      display " C= Unspecified Combin " at 12,50 attribute(reverse)
      exit case
    when cntlcmp = "U"
      display " U= Unknown " at 12,50 attribute(reverse)
      exit case
  end case
end function
#####

```


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FUNCTION cmpmeth_trans(cmpmeth)

define

cmpmeth char(20),

compmeth char(2)

let chosen = 1

case

when compmeth = "A1"

let cmpmeth = "NON-CROSSOVER"

exit case

when compmeth = "A2"

let cmpmeth = "ONE-WAY"

exit case

when compmeth = "A3"

let cmpmeth = "PARALLEL GROUP"

exit case

when compmeth = "B1"

let cmpmeth = "CROSSOVER"

exit case

when compmeth = "B2"

let cmpmeth = "LATIN SQUARE"

exit case

when compmeth = "B3"

let cmpmeth = "RANDOMIZED BLOCK"

exit case

when compmeth = "C"

let cmpmeth = "COMBINATION NOS"

exit case

when compmeth = "U"

let cmpmeth = "UNKNOWN"

exit case

otherwise

let cmpmeth = ""

error beep, "Not an acceptable choice!"

let chosen = 0

exit case

end case

return cmpmeth

end function

#####

FUNCTION cntlmeth_choice()

call clear_choice(8,16,50)

display "A = Concurrent " at 12, 50 attribute(reverse)

display "B = Non-Concurrent " at 13, 50 attribute(reverse)

display "N = None " at 14, 50 attribute(reverse)

display "U = Unknown " at 15, 50 attribute(reverse)

end function

#####

FUNCTION cntlmeth_trans(hold_cntlmeth)

define

hold_cntlmeth like stdydsgr.stycntlmeth,

tmp_cntlmeth char(20)

let chosen = 1

case

when hold_cntlmeth = "A"

let tmp_cntlmeth = "CONCURRENT"

exit case

when hold_cntlmeth = "B"

```

    let tmp_cntlmeth = "NON-CONCURRENT"
    exit case
  when hold_cntlmeth = "N"
    let tmp_cntlmeth = "NONE"
    exit case
  when hold_cntlmeth = "U"
    let tmp_cntlmeth = "UNKNOWN"
    exit case
  otherwise
    error beep, "Not an acceptable choice"
    let tmp_cntlmeth = " "
    let chosen = 0
    exit case
  end case
return tmp_cntlmeth
end function
#####
FUNCTION cntltyp_choice(stycntlmeth)
  define stycntlmeth char(1)
  call clear_choice(8,16,50)
  case
    when stycntlmeth = "A"
      display " A1 = Active Agent " at 12,50 attribute(reverse)
      display " A2 = Inactive Agent " at 13,50 attribute(reverse)
      display " A3 = No Agent " at 14,50 attribute(reverse)
      exit case
    when stycntlmeth = "B"
      display " B1 = Historical " at 12,50 attribute(reverse)
      display " B2 = Matched Pairs " at 13,50 attribute(reverse)
      exit case
    when stycntlmeth = "N"
      display " N = None " at 12,50 attribute(reverse)
      exit case
    when stycntlmeth = "U"
      display " U = Unknown " at 12,50 attribute(reverse)
      exit case
  end case
end function
#####
FUNCTION cntltyp_trans(cntltyp)
  define cntltyp char(2),
    stycntltyp char(20)

  let chosen = 1
  case
    when cntltyp = "A1"
      let stycntltyp = "ACTIVE AGENT"
      exit case
    when cntltyp = "A2"
      let stycntltyp = "INACTIVE AGENT"
      exit case
    when cntltyp = "A3"
      let stycntltyp = "NO AGENT"
      exit case
    when cntltyp = "B1"
      let stycntltyp = "HISTORICAL"
      exit case

```

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```
when cntltyp = "B2"
  let stycntltyp = "MATCHED PAIRS"
  exit case
when cntltyp = "N"
  let stycntltyp = "NONE"
  exit case
when cntltyp = "U"
  let stycntltyp = "UNKNOWN"
  exit case
otherwise
  error beep, "Not an acceptable choice!"
  let stycntltyp = " "
  let chosen = 0
  exit case
end case
return stycntltyp
end function
#####
FUNCTION cntlassgn_choice()
  call clear_choice(8,16,50)
  display " A = Randomized " at 12, 50 attribute(reverse)
  display " B = Matched Pair " at 13, 50 attribute(reverse)
  display " C = Arbitrary Assignment " at 14, 50 attribute(reverse)
  display " N = None " at 15, 50 attribute(reverse)
  display " U = Unknown " at 16, 50 attribute(reverse)
  end function
#####
FUNCTION cntlassgn_trans(cntlassgn)
  define
    cntlassgn char(2),
    stycntassgn char(20)
  let chosen = 1
  case
    when cntlassgn = "A"
      let stycntassgn = "RANDOMIZED"
      exit case
    when cntlassgn = "B"
      let stycntassgn = "MATCHED PAIR"
      exit case
    when cntlassgn = "C"
      let stycntassgn = "ARBITRARY"
      exit case
    when cntlassgn = "N"
      let stycntassgn = "NONE"
      exit case
    when cntlassgn = "U"
      let stycntassgn = "UNKNOWN"
      exit case
    otherwise
      error beep, "Not an acceptable choice!"
      let stycntassgn = " "
      let chosen = 0
      exit case
  end case
  return stycntassgn
end Function
#####
```

FUNCTION rte_choice()

```

call clear_choice(8,18,52)
display "PO = Oral " at 9,52 attribute(reverse)
display "SK = Dermal " at 10,52 attribute(reverse)
display "IH = Inhaled " at 11,52 attribute(reverse)
display "IV = IV Inj " at 12,52 attribute(reverse)
display "IM = IM Inj " at 13,52 attribute(reverse)
display "IA = IA Inj " at 14,52 attribute(reverse)
display "SQ = SQ Inj " at 15,52 attribute(reverse)
display "OC = Ocular " at 16,52 attribute(reverse)
display "BT = Bite-St " at 17,52 attribute(reverse)
display "UK = Unk " at 18,52 attribute(reverse)
end function

```

```
#####
```

FUNCTION rte_trans(rte)

```

define
    rte like exporegm.exroute,
    hold_rte char(20)
let chosen = 1
Case
    when rte = "PO"
        let hold_rte = "ORAL"
        exit case
    when rte = "SK"
        let hold_rte = "DERMAL"
        exit case
    when rte = "IH"
        let hold_rte = "INHALATION"
        exit case
    when rte = "IV"
        let hold_rte = "INTRAVENOUS INJ"
        exit case
    when rte = "IM"
        let hold_rte = "INTRAMUSCULAR INJ"
        exit case
    when rte = "IA"
        let hold_rte = "INTRA-ARTERIAL INJ"
        exit case
    when rte = "SQ"
        let hold_rte = "SUBCUTANEOUS INJ"
        exit case
    when rte = "OC"
        let hold_rte = "OCULAR"
        exit case
    when rte = "BT"
        let hold_rte = "BITE-STING"
        exit case
    when rte = "UK"
        let hold_rte = "UNKNOWN"
        exit case
    otherwise
        error beep, "Not an acceptable choice"
        let hold_rte = " "
        let chosen = 0
        exit case
end case
return hold_rte

```

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```
end function
#####
FUNCTION sex_choice()
  call clear_choice(9,13,50)
  display " M = Male " at 9,50 attribute(reverse)
  display " F = Female " at 10,50 attribute(reverse)
  display " C = Castrated Male " at 11,50 attribute(reverse)
  display " B = Both Sexes" at 12,50 attribute(reverse)
  display " N = Neutered Female " at 13,50 attribute(reverse)
  display " U = Unknown Sex " at 14,50 attribute(reverse)
end function
#####
FUNCTION sex_trans(sex)
  define
    sex char(1),
    rtn_sex char(20)
  let chosen = 1
  case
    when sex = "M"
      let rtn_sex = "MALE"
      exit case
    when sex = "F"
      let rtn_sex = "FEMALE"
      exit case
    when sex = "N"
      let rtn_sex = "NEUTERED FEMALE"
      exit case
    when sex = "C"
      let rtn_sex = "CASTRATED MALE"
      exit case
    when sex = "B"
      let rtn_sex = "BOTH SEXES"
      exit case
    when sex = "U"
      let rtn_sex = "UNKNOWN"
      exit case
    otherwise
      let chosen = 0
      let rtn_sex = " "
      exit case
  end case
  return rtn_sex
end function
#####
FUNCTION date_choice()
  call clear_choice(9,14,50)
  display " D = Days " at 9,50 attribute(reverse)
  display " W = Weeks " at 10,50 attribute(reverse)
  display " M = Months " at 11,50 attribute(reverse)
  display " Y = Years " at 12,50 attribute(reverse)
  display " U = Unknown " at 13,50 attribute(reverse)
end function
#####
FUNCTION date_trans(dte)
  define
    dte like subjgrp.sgageunit,
    rtn_date char(20)
```

```

let chosen = 1
case
  when dte = "M"
    let rtn_date = "MONTH(S)"
    exit case
  when dte = "D"
    let rtn_date = "DAY(S)"
    exit case
  when dte = "W"
    let rtn_date = "WEEK(S)"
    exit case
  when dte = "Y"
    let rtn_date = "YEAR(S)"
    exit case
  when dte = "Y"
    let rtn_date = "UNKNOWN"
    exit case
  otherwise
    let chosen = 0
    let rtn_date = " "
    exit case
end case
return rtn_date
end function
#####
function form_choice()
  call clear_choice(9,18,52)
  display " 01 = Solid " at 9,52 attribute(reverse)
  display " 02 = Slo_rel " at 10,52 attribute(reverse)
  display " 03 = Semisol " at 11,52 attribute(reverse)
  display " 04 = Liquid " at 12,52 attribute(reverse)
  display " 05 = Spray " at 13,52 attribute(reverse)
  display " 06 = Gas " at 14,52 attribute(reverse)
  display " 07 = Concent " at 15,52 attribute(reverse)
  display " 08 = Feed " at 16,52 attribute(reverse)
  display " 09 = Bait " at 17,52 attribute(reverse)
  display " 00 = Unk " at 18,52 attribute(reverse)
end function
#####
function form_trans(formul)
  define
    formul like exporegm.exformul,
    hold_formul char(20)
  let chosen = 1
  case
    when formul = "01"
      let hold_formul = "SOLID"
      exit case
    when formul = "02"
      let hold_formul = "SLOW-RELEASE"
      exit case
    when formul = "03"
      let hold_formul = "SEMI-SOLID"
      exit case
    when formul = "04"
      let hold_formul = "LIQUID"
      exit case

```

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```
when formul = "05"
    let hold_formul = "SPRAY"
    exit case
when formul = "06"
    let hold_formul = "GAS"
    exit case
when formul = "07"
    let hold_formul = "CONCENTRATE"
    exit case
when formul = "08"
    let hold_formul = "FEED"
    exit case
when formul = "09"
    let hold_formul = "BAIT"
    exit case
when formul = "00"
    let hold_formul = "UNKNOWN"
    exit case
otherwise
    error beep, "Not an acceptable choice"
    let hold_formul = " "
    let chosen = 0
    exit case
end case
return hold_formul
end function
#####
function severe_trans(hold_severe)
define
    hold_severe like clinfind.cfsevvalue,
    tmp_severe char(12)
let chosen = 1
case
    when hold_severe = 1
        let tmp_severe = "MILD"
        exit case
    when hold_severe = 2
        let tmp_severe = "MODERATE"
        exit case
    when hold_severe = 3
        let tmp_severe = "SEVERE"
        exit case
    otherwise
        let tmp_severe = "UNK SEVERITY"
        let chosen = 1
        exit case
end case
return tmp_severe
end function
#####
FUNCTION pur_choice()
call clear_choice(8,18,52)
display " TOX = Toxic " at 9,52 attribute(reverse)
display " TRT = Treat " at 10,52 attribute(reverse)
display " CNL = Control " at 11,52 attribute(reverse)
display " OTH = Other " at 12,52 attribute(reverse)
display " NON = None " at 13,52 attribute(reverse)
```

```

display " UNK = Unknown " at 14,52 attribute(reverse)
end function
#####
FUNCTION pur_trans(tmp_val)
define
    tmp_val char(3),
    hold_val char(10)
let chosen = 1
CASE
    when tmp_val = "TOX"
        let hold_val = "TOXIC"
        exit case
    when tmp_val = "TRT"
        let hold_val = "TREAT"
        exit case
    when tmp_val = "CNL"
        let hold_val = "CONTROL"
        exit case
    when tmp_val = "OTH"
        let hold_val = "OTHER"
        exit case
    when tmp_val = "NON"
        let hold_val = "NONE"
        exit case
    when tmp_val = "UNK"
        let hold_val = "UNK"
        exit case
    otherwise
        let chosen = 0
        let hold_val = " "
        exit case
end case
return hold_val
end FUNCTION
#####
FUNCTION dose_choice()
call clear_choice(8,18,52)
display " MG   = Milligrams   " at 9,52 attribute(reverse);
display " ML   = Milliliters  " at 10,52 attribute(reverse)
display " UG   = Micrograms   " at 11,52 attribute(reverse)
display " MG/KG = Milligram/Kg " at 12,52 attribute(reverse)
display " UG/KG = Microgram/Kg " at 13,52 attribute(reverse)
end function
#####
FUNCTION change_choice()
call alrt1940open()
display " 0 = NOS " at 5,8
display " 1 = NORMAL " at 6,8
display " 2 = DISORDER " at 7,8
display " 3 = INCREASE " at 8,8
display " 4 = DECREASE " at 9,8
display " 5 = ABSENCE " at 10,8
display " 6 = ABNRM PRESENCE " at 11,8
display " 7 = ABNRM RATIO " at 12,8
prompt "Enter number for change seen > " for answer
on key(interrupt)
call alrt1940close()

```


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```
        return
    end prompt
    call alrt1940close()
    return answer
end function
#####
function trans_change(tmp_cng)
    define
        tmp_cng char(1),
        hold_change like c'infind.cfchange
    case
        when tmp_cng = "0"
            let hold_change = "NOS"
            exit case
        when tmp_cng = "1"
            let hold_change = "NORMAL"
            exit case
        when tmp_cng = "2"
            let hold_change = "DISORDER"
            exit case
        when tmp_cng = "3"
            let hold_change = "INCREASE"
            exit case
        when tmp_cng = "4"
            let hold_change = "DECREASE"
            exit case
        when tmp_cng = "5"
            let hold_change = "ABSENCE"
            exit case
        when tmp_cng = "6"
            let hold_change = "ABNRM PRESENCE"
            exit case
        when tmp_cng = "7"
            let hold_change = "ABNRM RATIO"
            exit case
    end case
    return hold_change
end function
#####
FUNCTION matrix_choice()
    call alrt1940open()
    display "A - Blood   ~ at 3,4"
    display "B - Plasma  ~ at 4,4"
    display "C - Serum   ~ at 5,4"
    display "D - Milk    ~ at 6,4"
    display "E - Saliva   ~ at 7,4"
    display "F - Gastric Cntnt ~ at 8,4"
    display "G - Feces    ~ at 9,4"
    display "H - Vomitus   ~ at 10,4"
    display "I - Urine    ~ at 11,4"
    display "J - CSF      ~ at 12,4"
    display "Z - Other Matrix ~ at 13,4"
    display "X - Exit w/o Select ~ at 15,4"
    prompt "Enter letter for sample matrix >" for char answer
    on key (interrupt)
        call alrt1940close()
        let answer = "Z"
```

```

    return answer
  end prompt
  let answer = upshift(answer)
  call alrt1940close()
  return answer
END FUNCTION
#####
FUNCTION matrix_trans(tmp_value)
  define
    T_lab record
      loccode char(6),
      locname char(100)
    end record,
    tmp_value char(1)
  let chosen = 0
  Case
    when answer = "A"
      let T_lab.loccode = "T0X00"
      let T_lab.locname = "BLOOD"
      exit case
    when answer = "B"
      let T_lab.loccode = "T0X40"
      let T_lab.locname = "PLASMA"
      exit case
    when answer = "C"
      let T_lab.loccode = "T0X50"
      let T_lab.locname = "SERUM"
      exit case
    when answer = "D"
      let T_lab.loccode = "T0Y31"
      let T_lab.locname = "MILK"
      exit case
    when answer = "E"
      let T_lab.loccode = "T5X00"
      let T_lab.locname = "SALIVA"
      exit case
    when answer = "F"
      let T_lab.loccode = "T6Y00"
      let T_lab.locname = "GASTRIC CONTENTS"
      exit case
    when answer = "G"
      let T_lab.loccode = "T6Y10"
      let T_lab.locname = "FECES"
      exit case
    when answer = "H"
      let T_lab.loccode = "T6Y10"
      let T_lab.locname = "VOMITUS"
      exit case
    when answer = "I"
      let T_lab.loccode = "T7X10"
      let T_lab.locname = "URINE"
      exit case
    when answer = "J"
      let T_lab.loccode = "TX100"
      let T_lab.locname = "CEREBROSPINAL FLUID"
      exit case
    when answer = "Z"

```

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```
    call pick_site() returning T_lab.loccode, T_lab.locname
    exit case
otherwise
    let chosen = 1
    let T_lab.loccode = "Null"
    let T_lab.locname = "Null"
    exit case
end case
return T_lab.loccode, T_lab.locname
END FUNCTION
#####
FUNCTION system_choice()
    call alrt1940open()
    display "A - Circulatory" " at 3,4
    display "B - Digestive" " at 4,4
    display "C - Hemato / Lymph / Reticuloen" at 5,4
    display "D - Integumentary / Skin" " at 6,4
    display "E - Musculoskeletal" " at 7,4
    display "F - Nervous / Behavioral" " at 8,4
    display "G - Reproductive" " at 9,4
    display "H - Respiratory" " at 10,4
    display "I - Senses" " at 11,4
    display "J - Urinary" at 12,4
    display "K - General" " at 3,4
    display "L - Endocrine" " at 14,4
    display "M - Other/Immunologic/Metabol" " at 15,4
    display "Z - Exit without choosing" " at 17,4
    prompt "Enter letter for body system >" for char answer
    on key (interrupt)
        call alrt1940close()
        let answer = "Z"
        return answer
    end prompt
    let answer = upshift(answer)
    call alrt1940close()
    return answer
END FUNCTION
#####
FUNCTION system_trans(tmp_value)
    define
        T_sys record
            syscode char(8),
            sysname char(100)
        end record,
        tmp_value char(1)
    let chosen = 0
    Case
        when tmp_value = "A"
            let T_sys.syscode = "A"
            let T_sys.sysname = "CIRCULATORY"
            exit case
        when tmp_value = "B"
            let T_sys.syscode = "B"
            let T_sys.sysname = "DIGESTIVE"
            exit case
        when tmp_value = "C"
            let T_sys.syscode = "C"
```

```

    let T_sys.sysname = "HEMATOPOETIC-LYMPHATIC-RETICULOENDOTHELIC"
    exit case
  when tmp_value = "D"
    let T_sys.syscode = "D"
    let T_sys.sysname = "INTEGUMENTARY-SKIN"
    exit case
  when tmp_value = "E"
    let T_sys.syscode = "E"
    let T_sys.sysname = "MUSCULOSKELETAL"
    exit case
  when tmp_value = "F"
    let T_sys.syscode = "F"
    let T_sys.sysname = "NERVOUS-BEHAVIORAL"
    exit case
  when tmp_value = "G"
    let T_sys.syscode = "G"
    let T_sys.sysname = "REPRODUCTIVE"
    exit case
  when tmp_value = "H"
    let T_sys.syscode = "H"
    let T_sys.sysname = "RESPIRATORY"
    exit case
  when tmp_value = "I"
    let T_sys.syscode = "I"
    let T_sys.sysname = "SENSES"
    exit case
  when tmp_value = "J"
    let T_sys.syscode = "J"
    let T_sys.sysname = "URINARY"
    exit case
  when tmp_value = "K"
    let T_sys.syscode = "K"
    let T_sys.sysname = "GENERAL"
    exit case
  when tmp_value = "L"
    let T_sys.syscode = "L"
    let T_sys.sysname = "ENDOCRINE"
    exit case
  when tmp_value = "M"
    let T_sys.syscode = "M"
    let T_sys.sysname = "OTHER-IMMUNOLOGIC-METABOLISM"
    exit case
  when tmp_value = "Z"
    let T_sys.syscode = "null"
    let T_sys.sysname = "null"
    let chosen = 1
    exit case
  otherwise
    Error "Not acceptable system"
    let chosen = 1
    exit case
end case
return T_sys.syscode, T_sys.sysname
END FUNCTION
#####
FUNCTION labCatChoice()
  call alrt1940open()

```

Toxin Knowledge System Source Code

```
display " A - Elements/Ions/Inorganics/Acid-Base " at 3,1
display " B = Simple Organics/Carbohydrates " at 4,1
display " C = Proteins/Amino Acids " at 5,1
display " D = Fatty Acids/Lipids/Lipoproteins " at 6,1
display " E = Porphyrins/Bilirubin Cmpd/Bile Acids " at 7,1
display " F = Purines/Pyrimidines/Nucleic Acids " at 8,1
display " G = Vitamins " at 9,1
display " H = Hemoglobins " at 10,1
display " I = Enzymes " at 11,1
display " J = Endocrine Substances " at 12,1
display " K = Nervous System Substances " at 13,1
display " L = Immune System Substances " at 14,1
display " M = Hematopoetic Functions " at 15,1
display " Z = Exit without choosing " at 17,1
prompt "Enter letter for lab test category >" for char answer
    on key (interrupt)
        call alrt1940close()
        let answer = "Z"
        return answer
    end prompt
let answer = upshift(answer)
call alrt1940close()
return answer
END FUNCTION
#####
FUNCTION labCatTran(tmp_value)
define
    tmp_value char(1),
    T_sys record
        syscode char(8),
        sysname char(100)
    end record
Case
    when tmp_value = "A"
        let T_sys.syscode = "A"
        let T_sys.sysname = "Elements/Ions/Inorganics/Acid-Base"
        exit case
    when tmp_value = "B"
        let T_sys.syscode = "B"
        let T_sys.sysname = "Simple Organics/Carbohydrates"
        exit case
    when tmp_value = "C"
        let T_sys.syscode = "C"
        let T_sys.sysname = "Proteins/Amino Acids"
        exit case
    when tmp_value = "D"
        let T_sys.syscode = "C"
        let T_sys.sysname = "Proteins/Amino Acids"
        exit case
    when tmp_value = "E"
        let T_sys.syscode = "E"
        let T_sys.sysname = "Porphyrins/Bilirubin Cmpd/Bile Acids"
        exit case
    when tmp_value = "F"
        let T_sys.syscode = "F"
        let T_sys.sysname = "Purines/Pyrimidines/Nucleic Acids"
        exit case
```

```

when tmp_value = "G"
  let T_sys.syscode = "G"
  let T_sys.sysname = "Vitamins"
  exit case
when tmp_value = "H"
  let T_sys.syscode = "H"
  let T_sys.sysname = "Hemoglobins"
  exit case
when tmp_value = "I"
  let T_sys.syscode = "I"
  let T_sys.sysname = "Enzymes"
  exit case
when tmp_value = "J"
  let T_sys.syscode = "J"
  let T_sys.sysname = "Endocrine Substances"
  exit case
when tmp_value = "K"
  let T_sys.syscode = "K"
  let T_sys.sysname = "Nervous System Substances"
  exit case
when tmp_value = "L"
  let T_sys.syscode = "L"
  let T_sys.sysname = "Immune System Substances"
  exit case
when tmp_value = "M"
  let T_sys.syscode = "M"
  let T_sys.sysname = "Hematopoietic Functions"
  exit case
when tmp_value = "Z"
  let T_sys.syscode = "null"
  let T_sys.sysname = "null"
  let chosen = 1
  exit case
end case
return T_sys.syscode, T_sys.sysname
END FUNCTION
#####
function agern_choice()
  call clear_choice(9,14,50)
  display " 1 = Infant " at 9,50 attribute(reverse)
  display " 2 = Juvenile " at 10,50 attribute(reverse)
  display " 3 = Adult " at 11,50 attribute(reverse)
  display " 4 = Elderly " at 12,50 attribute(reverse)
  display " 0 = Unknown " at 13,50 attribute(reverse)
  end function
#####
FUNCTION agern_tran(t_arange)
  define
    t_arange  char(1),
    tmp_val   char(10)
  let chosen = 1
  case
    when t_arange = "0"
      let tmp_val = "UNKNOWN AGE"
      exit case
    when t_arange = "1"
      let tmp_val = "INFANT"

```

```

        exit case
    when t_arange = "2"
        let tmp_val = "JUVENILE"
        exit case
    when t_arange = "3"
        let tmp_val = "ADULT"
        exit case
    when t_arange = "4"
        let tmp_val = "ELDERLY"
        exit case
    otherwise
        let chosen = 0
        let tmp_val = " "
        exit case
    end case
return tmp_val
end FUNCTION
#####
function wt_choice()
    call clear_choice(9,14,50)
    display " LB = Pounds  " at 9,50 attribute(reverse)
    display " OZ = Ounces  " at 10,50 attribute(reverse)
    display " KG = Kilograms " at 11,50 attribute(reverse)
    display " GM = Grams    " at 12,50 attribute(reverse)
    display " UK = Unknown  " at 13,50 attribute(reverse)
end function
#####
FUNCTION wrangeChoice()
    define
        tmp_val char(2)
    open window wrange at 3,3 with 7 rows, 68 columns
        attribute(border, reverse)
    display "00 = None" at 2,1
    display "U = Unk " at 2,20
    display "M = Multi range" at 2,40
    display "01 = < 1 kg (< 2 lb) " at 3,1
    display "02 = 1 - 2 kg (>2-4 lb) " at 4,1
    display "03 = 3 - 5 kg (>4-11 lb) " at 5,1
    display "04 = 6 - 10 kg (>11-22 lb) " at 6,1
    display "05 = 11 - 25 kg (>22-55 lb) " at 7,1
    display "06 = 26 - 50 kg (>55-110 lb) " at 3,36
    display "07 = 51 - 100 kg (>110-220 lb) " at 4,36
    display "08 = 101 - 200 kg (>220-440 lb) " at 5,36
    display "09 = 201 - 500 kg (>440-1100 lb) " at 6,36
    display "10 = 501 - 1000 kg (>1120-2200 lb)" at 7,36
    prompt "Enter letter for weight range >" for tmp_val
        on key (interrupt)
            close window wrange
            let tmp_val = "U"
            return answer
        end prompt
    close window wrange
    let tmp_val = upshift(tmp_val)
    return tmp_val
end FUNCTION
#####

```

```
FUNCTION wtrgn_tran(t_wrgn)
  define
    t_wrgn char(2),
    tmp_val char(10)
  let chosen = 1
  case
    when t_wrgn = "00"
      let tmp_val = "None"
      exit case
    when t_wrgn = "01"
      let tmp_val = "< 1 kg"
      exit case
    when t_wrgn = "02"
      let tmp_val = "1 - 2 kg"
      exit case
    when t_wrgn = "03"
      let tmp_val = "3 - 5 kg"
      exit case
    when t_wrgn = "04"
      let tmp_val = "5-10 kg"
      exit case
    when t_wrgn = "05"
      let tmp_val = "11-25 kg"
      exit case
    when t_wrgn = "06"
      let tmp_val = "26-50 kg"
      exit case
    when t_wrgn = "07"
      let tmp_val = "51-100 kg"
      exit case
    when t_wrgn = "08"
      let tmp_val = "101-250 kg"
      exit case
    when t_wrgn = "09"
      let tmp_val = "250-500 kg"
      exit case
    when t_wrgn = "10"
      let tmp_val = "501-1000kg"
      exit case
    when t_wrgn = "U"
      let tmp_val = "Weight Unk"
      exit case
    when t_wrgn = "M"
      let tmp_val = ">1 Wt Rgn"
      exit case
    otherwise
      let chosen = 0
      let tmp_val = " "
      exit case
  end case
  return tmp_val
end FUNCTION
```


Toxin Knowledge System Source Code

#tkshelp.src

PLEASE NOTE: If you make changes in this file let me know! This is the back-up file. If I do not know specifically what you did, I can't identify the changes and insert them into the MASTER copy. Please communicate.

universal help, numbers 1-9
tksmain.4gl help, numbers 10-99
tkscit.4gl help, numbers 100-199
tksaauth.4gl help, numbers 200-299
tkscopy.4gl help, numbers 300-399
tkspapovr.4gl help, numbers 400-499
tksdsgn.4gl help, numbers 500-599
tksgpr.4gl help, numbers 600-699
tksexpo.4gl help, numbers 700-799
tksexgrp.4gl help, numbers 800-899
tksvoc.4gl and tksvoc2.4gl help, numbers 900-999
tksfinding.4gl help, numbers 1000-1099

File changed 02/24/89 RJL

Need to writ helps for
Monograph menu (TKS-MAIN REPORTS Abstract MONOGRAPH
)

UNIVERSAL HELP MESSAGES

- .1
No help available for this item.
- .2
Exit
Selecting this option will exit the current menu and take you to the previous window.
- .3 Hit ESC to leave array.
Hit the "Esc" key (and watch for an on-screen message) in order to begin the next step.
- .4
- .5
- .6
- .7
- .8
- .9

-1 tksmain.4gl HELP MESSAGES

.10

TKS-MAIN: (Overview)

When the TKS-MAIN window comes up, associated with it are the options available from that window. The first option is selected as indicated by the reverse video (highlighted or funnel enclosure < > on some screens) of "AbstractMgt."

Move through the menu by using the cursor keys. Note that moving through the menu in this fashion brings up brief messages which explain the highlighted option. Also, this method allows access to additional explanatory text available via on-line help messages which are accessed via simultaneously pressing the "control" and "w" keys (Ctrl-w).

You may invoke the desired option by typing (in lower case) the first letter of the option you wish to select, or by hitting "return." For example, typing "e" will select the "Exit" option. This method does not allow you to see the explanatory text which tells what the option will do. It is a short cut to speed up the process.

(Hit "s" or "return to see the help file for AbstractMgt)

TKS-MAIN: AbstractMgt

Selecting this option brings you to the "ABSTRACT" menu where abstracts can be entered, abstracts already entered can be added to (completed), or modified in some other way, or where searches for abstracted information can be performed.

.11

TKS-MAIN: Vocabulary

This option allows access to the lists and codes for journals, books, keywords, clinical findings and chemical vocabulary. These areas can be "browsed" (searches performed, entries modified or added to).

.12

TKS-MAIN: Reports

This section will be used to generate report summaries (monographs), but is not yet "on-line."

.13

TKS-MAIN: Information

This section contains the copyright notes and a summary of the stage of development of the individual programs which form the Toxin Knowledge System.

.14

TKS-MAIN: Exit

Selecting "Exit" removes you from the TKS program if you are in the first menu (TKS-MAIN), and moves you to the previous menu if you are at any other point in the program.

.15

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT: Results
Selecting "Results" brings up a menu of the same name with the option ClinicalFindings.

.16

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT: Discussion
This option is not yet on-line.

.20

TKS-MAIN ABSTRACT: New
Selecting "New" from this menu starts the process of entering a new citation. The screen which appears after "New" is selected prompts you for the last name of the first author of the article (type in lower case letters).

Please note that if you make a mistake, the "Back Space" key can be used. If you wish to abort an entry, use the "Del" (delete) key.

.21

TKS-MAIN ABSTRACT: Add
"Add" provides a means for adding to incomplete citation entries. For example, one can add descriptions of Designs, Subject Groups, Exposure Regimens and establish Links.

Selecting "Add" brings you to the "SELECT-FILE-BY" screen.

.22

TKS-MAIN ABSTRACT: Find
This option provides the capability of locating citations or any aspect of their associated data, i.e. designs, subject or exposure regimen information, clinical findings, comments, etc. Once the desired area is located, various options are available which allow the user to examine the records, modify or delete them.

.23

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT:
PaperOverview - Paper Overview data exists for this Paper.
Do you want to update it? (Y/n)
When you have chosen to "Add" paper overview data for a citation and the citation already has it, the system asks if you would like to update what is already there. Typing "y," followed by a "return," brings up the PAPER OVERVIEW SCREEN.

.30

TKS-MAIN VOCABULARY: Journals/Books
This option is used to add new journals or books to the source code list.

.31

TKS-MAIN VOCABULARY: Keywords
Selecting this option brings up the KEYWORD_LISTING menu with options to "Add" keycodes and keywords to the system memory, "Find" the keycode for a specific keyword or the keyword associated with a specific keycode.

.32

TKS-MAIN VOCABULARY: Signs

This function is not yet implemented.

.33

TKS-MAIN VOCABULARY: Chemicals

This function is not yet implemented.

.40

TKS-MAIN REPORTS: Journal-Listing

This option is used to print out the list of journals and source codes currently included in the TKS system file.

DO NOT USE THIS OPTION. It is under development.

.41

TKS-MAIN REPORTS: Abstract

This option is used to generate structured abstracts (monographs) for citations which are selected by the user. Selection of this option brings you to the Select-File-By screen in order to define the citation for which an abstract is to be generated.

THIS OPTION SHOULD NOT BE USED. The monograph section is under development.

.42

TKS-MAIN ABSTRACT SELECT-FILE-BY

From here, one can search for a specific citation by responding to sequential screens which request the author, the journal volume number, the first page number, and last two digits of the year. Alternatively, one can give the Citation No. which consists of the source code of the journal or book, the volume number, first page number, and the year. Note that for the latter, each component must consist of a certain number of characters, for example, J00001-0001-00001-1988.

Completion of the process will result in finding the desired citation, or a message that the citation doesn't exist in the database. If a citation isn't in the system, you can't add anything to it. Enter a new citation by starting from "New" in the "ABSTRACT" screen.

Hit "s" or "return" to see the help file for Author-Name.

TKS-MAIN ABSTRACT SELECT-FILE-BY: Author-Name

Type "a" or hit "return." Enter the first author's last name and hit "return." Now the program prompts you for the volume or chapter number. You must answer all of the questions posed by this path in order to search for a particular citation.

.43

TKS-MAIN ABSTRACT SELECT-FILE-BY: Author's Last Name

Enter only the first author's last name NOT the initials (case doesn't matter).

.44

Toxin Knowledge System Source Code

TKS-MAIN ABSTRACT SELECT-FILE-BY: Volume/Chapter Number

Enter the volume or chapter number followed by "return."

.45

TKS-MAIN ABSTRACT SELECT-FILE-BY: Citation-Number

Selecting this option results in a prompt asking for the citation number on which to do the search.

.46

TKS-MAIN ABSTRACT SELECT-FILE-BY: Which Citation-Number?

Type in the j or b and the following 5 numbers, a hyphen and the next 4 numbers, a hyphen and 5 numbers for the first page, a hyphen and the year, then "return" (remember, the format is J00001-0001-00001-1988).

The program either finds a match and brings up the menu asking what you would like to add, finds a match and tells you all data has been entered, or doesn't find a match and lets you know that too. Make sure you have typed the citation number correctly before trying to enter new citation information (via the "New" path if no match was found).

Respond to the prompts and you will come to the "ADD-DATA" screen if the citation is not already in the system.

.50

TKS-MAIN ABSTRACT FIND-DATA: Citation-Data

This option brings you to the FIND-CITATION-DATA screen where there are multiple methods of locating a particular citation or author.

.51

TKS-MAIN ABSTRACT FIND-DATA: Paper Content

"Paper Content" refers to the paper overview, materials and methods (design, subject, regimen and link information), results (clinical findings) and discussion portions of paper entries. Using this option, one can search for any of those areas of a paper which has already been entered. In addition, selection of this option provides a means of adding one or more of those specific entities if they are found to be missing after a query, by using the "Add-Data" option.

.52

TKS-MAIN ABSTRACT FIND-DATA: Keywords-Notes

Selection of Keywords-Notes brings you to the Find-Keywords-Notes menu where one can search for keywords or comments for a specific citation. The "Query All" option is also available from this window. It allows one to bring up additional details during a search, for example, the author(s) and title of the article.

.53

TKS-MAIN ABSTRACT FIND-DATA FIND-KEYWORDS-NOTES: Keywords

Selection of the "Keywords" option enables one to search for the keywords that have been entered for a particular citation. The screen comes up with the cursor on the "Citation" field and a message asking you to "Enter search criteria and hit ESC to Search." Provide the citation number (or the Citation File

Number, or a Keyword) and hit "Esc." If the citation exists in the system, and if Keycodes/Keywords were assigned, they will appear. When located, they may be modified or deleted. If none have been entered, they may be added to the record.

Watch for messages on-screen indicating what you should do. Typically, a message will come up asking you to hit "ESC" to continue, after which a "BROWSE" menu will appear. There are on-line help messages available for that menu.

.54

TKS-MAIN ABSTRACT FIND-DATA FIND-KEYWORDS-NOTES: Notes
The "Notes" option provides a mechanism for locating the comments entered in association with a particular document. The notes may be modified or deleted, or added if not found.

.55

TKS-MAIN ABSTRACT FIND-DATA FIND-KEYWORDS-NOTES: Query-All
The "Query-All" option enables one to search using citation attributes, the document title, author(s) or keywords. When a search is successful, those other portions of the screen are also provided.

.60

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA: Citation-Data
One can add citation information to the system using this path. More commonly, this would be done via the "New" option in the "ABSTRACT" window.

Even though this is an "ADD" path, a "Find" option becomes available which allows the user to search for abstract components.

.61

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA: Paper-Content
The "PAPER-CONTENT" screen which appears next requires that one select the type of data which will be entered. Choose one of the available options.

.62

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA: Keywords-Notes
Selecting this option allows you to add either additional keywords or notes (comments), depending on what is selected from the next menu.

.63

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CITATION-DATA: Citation
Selecting "Citation" allows you to add citation data to the system. Usually you would do this via the "TKS-MAIN AbstractMgt ABSTRACT New" path. However, if the citation portion of an entry is deleted, leaving the other components, this option can be used to re-enter the citation data.

.64

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CITATION-DATA: Authors
One can add authors to a partially completed list or add authors to a citation that lacks that attribute.

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If there are authors already listed for the citation, you can move through them with the cursor keys. You cannot change anything or add names until the "Esc" key is used.

After hitting "Esc" the message at the bottom of the screen changes and the cursor field is in reverse video (dependant on your terminal type). You can now make changes in the fields already entered or add names to the list. Remember, the program will correctly number the authors if you enter them in sequence.

When you are finished with the changes/additions, hit "Esc" to place them in the system memory.

(This help message is also available if you choose "Authors."

.65

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-KEYWORDS-NOTES: Keywords

Selecting "Keywords" brings up the keycode/keyword screen which enables one to add keywords to the specified document data.

.66

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-KEYWORDS-NOTES: Notes

Selecting "Notes" brings up the TKS "Comments" screen so that comments can be added to the specified document.

.69

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT: PaperOverview

Selecting "PaperOverview" will enable one to add that portion of the paper content to the citation information in the system.

PaperOverview consists of the stated and implied purpose, the paper class, and number of study designs.

.70

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT:

Materials-Methods

If the document entry process is complete through Paper Overview, one can add design, subject, regimen and link information by selecting this option.

Design information includes, the type of study, the number of subject groups and exposure regimens, information on controls and group comparisons.

.71

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT MATERIALS-METHODS:

Design

When you select design, the system checks to see if the number of designs that have been entered matches the number of designs indicated in the PAPER OVERVIEW SCREEN. If they do not, you must change the data in the overview screen to allow for entry of another design.

If there are fewer designs entered than the overview screen indicated there should be, a design screen will come up. Fill in the options as the cursor moves to each field. "Esc" brings up the next design screen.

.72

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT MATERIALS-METHODS:

Subjects

When this option is selected (assuming that the Design(s) have already been entered), the program asks which design you would like to add subjects to. The design(s) are shown mid-screen. Choose a number from the left margin and hit "return."

If you select a design for which all subject group information has been entered, you cannot enter another subject group. The system will return you to the MATERIALS-METHODS menu. If a subject group is lacking for the design you selected, a new SUBJECT GROUP SCREEN comes up and can be completed. Subject data includes information on the species, age, sex, weight and similar attributes.

.73

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT MATERIALS-METHODS:

Subjects-For which design?

If the document entry process is complete through Paper Overview, and all subject groups have not been entered, one can add design information by selecting the appropriate design.

.74

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT MATERIALS-METHODS:

Regimens

Selecting this option allows entry of agent, dose and dosing schedule information via the EXPOSURE REGIMEN DATA SCREEN.

.75

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT MATERIALS-METHODS:

Regimens-For which study design?

The designs already entered are listed numerically mid-screen, along with the number of subject groups already entered for each design, the number of exposure regimens for each, and whether a control group was included.

This option will work only if a regimen description is lacking for a design. Type in the design number that requires additional regimen(s) and hit "return." A new EXPOSURE REGIMEN DATA SCREEN appears.

.76

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT: FindData

This option provides a mechanism to access the "Find" path from the Add pathway. It brings you to another menu where the type of information you wish to find must be chosen (Citation, Paper Content and Keywords-Notes).

.77

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT: Links

Once the design, subject and regimen data are complete for a citation, one can establish the relationships between those factors using the "Link" screen. This option provides that capability.

.78

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT RESULTS:

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ClinFindings

The clinical findings reported in a document can be entered using this path. Clinical Findings currently involves describing the site affected, the structural change, functional alteration, causal agent and procedural, preventive, diagnostic and therapeutic measures.

.79

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT: Discussion

This section is under development. Discussion refers to the "Discussion" portion of manuscripts.

.80

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA: Citation

In order to locate a citation, one can specify a citation number, author(s), journal volume number and other attributes, or Query for all of those. The options available in the FIND-CITATION-DATA window allow a choice between those various methods. Also available is an option which presents the citations and associated information in a different format, which is for use by system programmers (Raw-Citation).

Select "Citation" and the familiar citation screen appears. Enter the citation number and hit "return" to initiate the search. If the citation is found, a "BVROWSE" menu appears which allows one to view or modify the matches discovered by the search (Find) process.

.81

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA: Authors

Selecting this option allows you to search for an author of a specific citation, or all articles which include a specific person as an author. You can only use one name in the search.

This screen comes up with the cursor on the "Citation No." field. You have indicated that you would like to find an author so you probably don't want to institute the search process based on that number. Move through the fields using the "return" or cursor keys until the cursor is in the first author field. Type in the name of the author (including initials!) whose citations you wish to locate, and hit "Esc" to initiate the search process.

You can search for all "Smith's" regardless of their initials, by using the wild card (*), e.g., "SMITH*." When wishing to find all documents authored or co-authored by a particular individual it may be preferable to use the wild card in place of both initials because some journal articles may not provide the names with both initials. Some system users may not choose to enter both initials. Some may ignore the plea to NOT place spaces between the initials, which means an exact match would need to have both initials matched as well as the spacing! A search using the first initial and a wild card will pick up all the single and double initials, regardless of the spacing. However, be aware that you must pay attention to the initials in order to weed out any matches that aren't exactly the author of interest.

If a match is found, a BROWSE screen appears which provides

you with several options.

.82

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA: Query-All

Selection of "Query-All" results in a screen which provides the usual mechanism of searching by use of the citation or file number, an author(s), title, or keyword(s). If a match is found, these other attributes are displayed on the screen too.

.83

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA: Raw-Citation

This option invokes another program which provides access to data in the TKS System. It is meant to be used by system developers and consists of data fields and their abbreviations. It is necessary to be familiar with the screens in the TKS System in order to interpret the abbreviations.

One can access citation and other data from the Raw-Citation option (different table types which can be seen by using the "Detail" and "Master" options available in the Perform screen).

.84

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA: Data-Add

The addition of this option to the menu provides a ready means of adding citation data to a partially completed system entry. With this option, it is not necessary to exit out to the "Add" option in order to add citation information.

Please note that one cannot finish a partially completed data screen using "Data-Add." In order to do that one must first "Find" the entry of interest and then "Update" it via the BROWSE menu.

.90

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT: PaperOverview

If a match is found after selection of "PaperOverview," then the stated purpose, implied purpose, paper class and number of study designs will be shown if they were all previously entered. If no match is found, and citation data has been entered, one is given the option to add these parameters to the citation.

.91

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT MATERIALS-METHODS: Design

Selection of this option provides a means to search for the experimental design attributes of a specific paper. This includes such things as the type of study, whether or not controls were used, how experimental groups were compared and assigned, and the number of subject groups and regimens.

One can search for a specific citation or any parameter associated with the data fields. The system will perform multiple matches, that is, you can enter several attributes and the system will search for designs which match all of the specifications.

Move through the data fields using the "return" or cursor keys.

.92

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TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT MATERIALS-METHODS: Subjects

Selecting "Subjects" brings up a blank subject screen and allows a search for a specific citation's subject(s) data. If a match is found, the subject data for each group can be examined and modified, if needed. If a match is not found, but the citation data is, subject data can be added via "Add-Data" in the FIND-CONTENT menu.

You can specify several subject features and the system will search for subject groups which match all of the specifications.

Move through the data fields using the "return" or cursor keys.

.93

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT MATERIALS-METHODS: Regimens

Selecting "Regimens" brings up a blank regimen screen and allows a search for a specific citation's regimen(s) or citations which have specific regimen attributes. If a match is found, the regimen data for each group can be examined and modified, if needed.

If a citation is found which is missing regimen data, it can be added via "Add-Data" in the FIND-CONTENT menu.

Move through the data fields using the "return" or cursor keys.

.94

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT MATERIALS-METHODS: Links

Links define the relationships between the exposure groups, design factors, subject characteristics and regimen parameters. By using the citation or file number, one can locate the links for a specific citation, as long as they are already in the system. Once found they can be updated (modified), or deleted. If not present, they can be added to the system via the Add-Data option in the FIND-CONTENT menu.

.95

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT: Add-Data

When attempting to locate a specific portion of a paper (Design, Subject Group, Regimen, etc.), one may get a message that it doesn't exist. If the document is at hand, the missing item(s) can be added using the Add-Data option. Without this capability in the FIND-CONTENT menu, one would have to exit out to the ABSTRACT menu and select the Add path.

.96

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT RESULTS: ClinicalFindings

This option allows one to locate the clinical findings associated with a citation. When found, they may be edited or deleted. If not present, they may be added via Add-Data in the FIND-CONTENT menu.

.97

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT: Ugly-View

This option is used by the system programmers.

.98

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CONTENT: Results

"Results" refers to Clinical Findings, which can be accessed via this menu choice.

.99

TKS-MAIN ABSTRACT FIND-DATA FIND-CONTENT: Materials-Methods

Selecting this option brings the user to a menu of the same name which provides access to design, subject, regimen and link data.

.-1 tkscit.4gl HELP MESSAGES

.100

CITATION DATA SCREEN: Source

You are asked for the journal (or book) "source code" which is a 5 digit number with a "J" (or "B") prefix. Make sure you begin with a "J" or "B" prefix!! (Please note that if you make a mistake, the "Back Space" key can be used. If you wish to abort an entry, use the "Del" [delete] key.)

You are not likely to know the source code for a particular journal, so the system provides help. (Hit the F5 key [function key 5] if your entry is a journal or the F6 key if it is a book.)

.101

CITATION DATA SCREEN: File Loc.

"File Loc." is an abbreviation for file location. This provides a way to indicate where a specific file may be located, and is particularly useful when files may be stored in several different locations. If one wants to locate a particular file, the TKS CITATION DATA SCREEN can be used to identify where to look (hopefully, it will be there).

Abbreviations can be set-up for particular places or names of individuals, since there is space for only 6 characters. Type in the location of the citation or book and hit "return."

If you do not wish to use this option, hit "return" to move to the next entry point.

.102

CITATION DATA SCREEN: Volume/Chap

Enter the volume of the journal or the number of the book chapter from which the article was taken, then hit "return" to move to the next field.

.103

CITATION DATA SCREEN: Pages

Enter the beginning page number followed by a "return," and the ending page number and "return." If there is only one page, skip the second field by hitting "return."

.104

CITATION DATA SCREEN: Year

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Enter the year in which the citation was published, using all four digits, then "return." If you are not in a hurry, try entering just the last two digits of the year then return. See what happens? An error message will occur if the year entered is less than 1000 or greater than the current year.

Completing this field correctly provides the program with the final bit of information necessary to construct the citation number ("Citation No"), which appears after the "return." This consists of the journal source code (6 spaces), the volume or chapter number (4 spaces), the beginning page number (5 spaces) and the year (four digits). All items must be separated by hyphens (e.g. J00001-0001-00001-1988).

The Citation No. can be used to locate files in other environments (Paper overview, Subject, Regimen, Links, etc.). When used in this

manner, the number must include characters in all of the spaces allotted, meaning that zero's should be used to fill in blank characters at the beginning of the field. Each field is separated by a hyphen (e.g. J00001-0001-00001-1988).

.105

CITATION DATA SCREEN: Title

Enter the title of the article (type in small case) with no period. There is room for even lengthy titles. They will not automatically wrap around the allotted space. As a result, words may be split at the end of lines. Do not try to override this feature.

The program does not correct spelling, so check your entry. Once the title is complete so is this screen, so hit "Esc," which causes what you typed to be written to memory.

.106

TKS-MAIN ABSTRACT FIND-DATA J-LIST: Find.1 JLIST DATA SCREEN

This option is used to help locate the proper source code for the journal in which the article you are abstracting appeared.

Select "Find" and type in what you believe the correct abbreviation would be for that journal. As an example, type TOXICOL APPL PHARM and hit the "escape" key (Esc). The program searches for a match.

NOTE: Return to this help message after trying the above. Do not look at the second screen of this help message now. If you elect to try this, keep referring to the help messages or the hardcopy of the program documentation.

TKS-MAIN ABSTRACT FIND-DATA J-LIST: Find.2 JLIST DATA SCREEN

As you can see, sometimes a match is not found. When this occurs you can try another series of letters or use an aid such as a "wild card" (*). Try typing in "TOX*" and then "return." Note that this time the system found a match, and the correct abbreviation is "TOXICOL APPL PHARM." Notice also that there are several other potential matches. Use the up and down arrow keys to move through the list until you come to the selection you desire.

Hit "Esc" to exit from that window and bring you back to the abstract window, where the system automatically enters the correct journal source code!

.107

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA J-LIST: Add JLIST DATA SCREEN

This option is used to add new journals to the source code list and assign them a source code number.

Type "a" and the TKS JOURNAL LIST SCREEN pops up with the cursor on the "Journal Name" field.

.108

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA J-LIST: Select JLIST DATA SCREEN

This option can be used after you have a list of journal abbreviations from which one must be selected. Its use requires that you hit delete after a list is generated, and then hit "Select," after which the user must highlight the desired abbreviation, and hit "Esc" as requested on screen.

Note that the same process can be accomplished with fewer steps using the "Find" option.

.109

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA B-LIST: Find.1 BLIST DATA SCREEN

This option is used to help locate the proper source code for the book in which the article you are abstracting appeared.

Select "Find," type in what you believe the correct abbreviation would be for that book and hit the "Escape" key (Esc). The program searches for a match.

If you elect to try this, keep referring to the help messages or the hardcopy of the program documentation.

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA B-LIST: Find.2 BLIST DATA SCREEN

Sometimes a match is not found. When this occurs you can try another series of letters, or use an aid such as a "wild card" (*). Try typing in a portion of the title, add a "*" and then hit "return."

If there are several matches, use the up and down arrow keys to move through the list until you come to the selection you desire.

Hit "Esc" to exit from that screen and bring you back to the abstract window, where the system automatically enters the correct journal source code!

.110

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA B-LIST: Add

This option is used to add new books to the source code list and assign them a source code number.

Type "a" and the TKS BOOK LIST screen pops up with the cursor on the "Book Title" field.

.111

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA B-LIST: Select

This option is to be used after you have a list of book abbreviations from which one must be selected. When this is the case, choose this option, highlight the desired abbreviation, and hit "Esc" as requested on screen.

The same process can be accomplished with fewer steps using the "Find" option.

.112

CITATION DATA SCREEN: Citation No.

Typing "return" again, fills in the "File No." field automatically. It consists of the first four letters of the first author's last name, the journal or chapter number, the beginning page number and last two digits of the year. This number may also be used to find the file after it is entered into the system. It does not consist of extra characters or spaces. There are periods separating portions of the entry (e.g. SMIT.10.23.1988)

If the citation you are attempting to enter is already in the system, you will receive notification of that fact. You may make changes in a file that is already in the system, but not from the "New" citation pathway.

If the citation is a new one, "Exit" back to the "ABSTRACT" window and begin the entry process. If the citation is not in the system, hit "retrun" to move to the title entry field.

.170

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE:

FIND-CONTENT MATERIALS-METHODS
FIND-CONTENT RESULTS
VOCABULARY JOURNAL-VOCABULARY
VOCABULARY BOOK-VOCABULARY
VOCABULARY KEYWORD-VOCABULARY
SIGN-VOCABULARY

Next, Previous, First, Last

The BROWSE menu appears as a result of a search process. It provides mechanisms for moving between components when more than one is found (Next, Previous, First and Last) a method for changing entries (Update), removing components (Delete), performing another search process (Query-Again) and exiting from the BROWSE menu (Exit).

.171

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Update

FIND-CONTENT MATERIALS-METHODS
FIND-CONTENT RESULTS
VOCABULARY JOURNAL-VOCABULARY
VOCABULARY BOOK-VOCABULARY
VOCABULARY KEYWORD-VOCABULARY

The "Update" option provides a means for changing any component in a window and, hence, the database entry. This is necessary when a component has been incorrectly or incompletely entered.

"Update" allows you to add or delete data. To add data to the end of a list, scroll through it using the down arrow key until an empty author field is reached. Then, type in the data followed by an "Esc."

If you have a list of data and need to place an entry in the middle of a list, put the cursor on the line below where you would like it added and hit the "F1" key. A new line will be opened and you can type in the new entry followed by an "Esc," which will write it to memory.

To delete an entry you must place the cursor on the line you would like to delete and hit the "F2" key. The line will be deleted, and after an "Esc," the changes will be written to memory.

.172

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Delete

This is a particularly powerful option which should be used carefully. When selected, the DELETE-JOURNAL-CIT menu comes up.

.174

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE

DELETE-JOURNAL-CIT: (Overview)

"Options"

The DELETE-JOURNAL-CIT menu comes up with options to delete a single screen (This-Table) or all screens linked to that citation (All-Tables).

(Hit "return" or "s" to see the help file for "This-Table")

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE

DELETE-JOURNAL-CIT: This-Table

Selecting this option will remove from the database all the data shown on-screen and return the user to the BROWSE menu.

.175

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE

DELETE-JOURNAL-CIT: All-Tables

Selecting this option will remove from the database all of the data shown on screen and all of the data associated with all other screens for this citation (e.g., Paper Overview, Design, Subjects, Regimens, Links, Clinical Findings, Comments, etc.).

The program gives a message on-screen each time a component has

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been removed. You can neither reverse the process once it has started nor recover the data once it has been removed.

When the delete process is finished, the user is returned to the BROWSE menu.

.176

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Query-Again

If you would like to perform another search this option will allow immediate access to the screen for entry of another search parameter without having to exit out all the way back to the "Find" option in the ABSTRACT menu.

.-1 tksauth.4gl HELP MESSAGES

.200

AUTHOR DATA SCREEN

Enter the last name, a space and initials (no space between initials) of the first author as requested in the note on the bottom of the screen. Hit "return" and the cursor moves to the "sequence" area where you can enter the correct position of the author in the sequence of names on the publication. You can add up to six names to the author list.

When you are finished, hit "Esc" once again. This writes to memory the author list and the keyword screen pops up.

.205

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Delete (Authors)

This is a particularly powerful option which should be used carefully. When selected, a question pops up asking if you would "like to Delete ALL author entries for this Citation." Respond (y for yes, n for no) and hit "return."

If you need to delete one (or fewer than all of the entries) use the "Update" option. Scroll through the author list using the cursor keys, and use the "F2" key to delete a specific author.

.-1 tkskey.4gl Help Messages

.300

TKS-MAIN ABSTRACT: KEYWORD DATA SCREEN (Overview)

Hit "return" TWICE to go directly to the help for KeyCodes.

KeyCodes and Keywords can be used to enter specific information on any aspect of a paper. Clinical signs, physical signs, gross pathology, clinical pathology and histopathology findings, toxin preparation methods, animal treatment information, statistical

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analysis or any other similar component of a report.

Keywords provide more than ancillary information. They can be used to search for certain papers that meet particular criteria. Which papers report effects of toxin X in monkeys? Who gave feed contaminated with purified toxin? Cultured extracts? Which papers reported the use of fasted mice and which allowed access to food up until the time of dosing? Do young animals react differently than older ones?

KeyCodes are used to simplify the entry process by decreasing the number of keystrokes needed to enter a description.

The current keycodes were designed primarily for use with journal or book articles describing toxicologic studies with mycotoxins, though they would be suitable for describing work with other toxins. They are arranged by major headings (toxin type, species, exposure route, etc.)

NOTE TO USERS! This portion of the program is under development. We are exploring "cleaner" easier ways to enter and use keywords. We would prefer that the program excerpt pieces of data that are entered as part of the other data modules and generate its own keyword list rather than the user having to look up what keycode goes with each keyword. This will take some effort. Until that is possible, what is currently available can be used.

Hit "return" to go directly to the help for KeyCodes.

KeyCodes

Enter the appropriate keycode(s) and hit "return." The keywords now appear to the right. Hit "Esc" to write them to memory.

If you do not wish to enter keycodes/keywords at this time, hit the "delete" key.

Since you probably do not know what the keywords are, enter a code of "C02" and press "return." The keyword matching that code is placed in the next field. If one knows the keywords, this is the quickest way to enter them. It may be useful to have a hard copy of the lists in order to look them up "manually" by major heading and group. If an incorrect entry is placed in the keycode field followed by a "return," or you hit the "delete" key, the program assumes you need help, and brings up the KEY-LIST SCREEN.

When you are finished with the KEYWORD DATA SCREEN the next screen has a menu title of "CURRENT PAPER" and has only one option, "Exit." That is because you are finished with the citation portion of the abstract and must begin the next phase of data entry. Hit "E" or "return" to go on. You are then asked if you would like to "add content data for the paper."

If you type "n" then "return," the system goes back to the "Abstract" screen. Typing "y" followed by "return" results in a new screen which begins the paper overview process.

.B 301

TKS-MAIN ABSTRACT FIND-DATA FIND-KEYWORDS-NOTES: Keywords

This pathway provides a means of listing all the keywords that have been entered for a particular citation. The screen comes up with the cursor on the Citation field and a message asking you to "Enter search criteria and hit ESC to search." Provide the citation number (or the Citation file number) and hit "Esc." If the citation exists in the system, and if keycodes/keywords were assigned, they will appear.

Watch for messages on-screen that will indicate what you should do. Typically a message will come up asking you to hit "Esc" to continue, after which a "BROWSE" menu will appear. There are on-line help messages available for that menu.

.302

TKS-MAIN ABSTRACT KEY-LIST: Find

The "Find" option helps you search for particular keywords that are in the keyword list, and identifies their associated keycode.

The following is an example:

Type "f" and the cursor is placed on the first field (keycode). Hit "return" and the cursor goes to the next field. Type in the word "mouse" and hit "Esc." The program searches for that keyword and, if it is found, fills in the keycode number. One can complete those two fields for the paper being abstracted by hitting "Esc" once again. From there the process starts over for the next keyword. (The process can be aborted by hitting the delete key unless "Exit" is available in the menu.)

If a keyword is searched for but not found, the program responds with the message that "There is no keyword matching the first three letters" and returns you to the original screen. If that occurs and you would like to add a keyword to the list, select "Add" in the KEY-LIST menu.

.303

TKS-MAIN ABSTRACT KEY-LIST: Add

The "Add" option allows the freedom to associate new or additional keywords with a citation. If you do not wish to enter keywords at this time, hit the "delete" key when you are in the KEYWORD DATA SCREEN. (If you follow this later path, the screen indicates that it is preparing citation "information.")

.305

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA FIND-KEYWORDS-NOTES
BROWSE: Delete (Keywords)

This is a particularly powerful option which should be used carefully. When selected, the user is asked if they would like to "Delete ALL keyword entries for this Citation." Respond (y for yes, "n" for no) and hit "return."

Delete removes ALL of the keywords. If you need to delete one (or fewer than all of the entries) use the "Update" option.

-1 tkspapovr.4gl Help Messages

.400

PAPER OVERVIEW SCREEN: Stated Purpose

There is room here to succinctly identify the stated purpose of the paper or book. That is, the purpose as stated by the authors. There are 50 spaces. Type in the stated purpose followed by "return."

.401

PAPER OVERVIEW SCREEN: Implied Purpose

One can often identify information which hints at a purpose not specifically stated. For example, researchers may study the effects of an expensive toxin on mice, because they do not have enough material to use on a larger animal that may be more closely related to the target population, people. Or, the long term effects of a toxin such as cadmium may be the primary interest, but animals were only fed contaminated diets for 2 weeks because they developed a viral infection and began to die.

Type in the implied purpose followed by "return." If there is none, leave it blank (hit "return").

.402

PAPER OVERVIEW SCREEN: Paper Class

Select one of the descriptors from the pop-up menu on the right side of the screen by typing the indicated letter in the space provided.

Paper Class; First Field (hit "return" TWICE to see the second field help)

E= Experimental: Includes documents which report the results of experiments which have been performed. This category includes both in vivo and in vitro studies.

N= Non-Experimental: Documents in this category may include the following:

1. Clinical case reports which detail circumstances of exposure, results, effects of treatment on the outcome, and suggestions for preventing future exposures.
2. Epidemiology reports which look at causes and effects in either a retrospective or prospective direction.

I= Info Only: These may include literature reviews or comments such as letters to editors.

C= Combination: As the name suggests, this category includes documents which contain more than one type of paper class.

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When you complete that field the cursor moves to the next one and the descriptors change. Enter the appropriate classification and the cursor will move to the next field.

Hit "s" or "return" to view the help for the second field.

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Help 412 Paper Class Choices; Second Field

E10= Toxicity: Refers to the study of the toxic effects of compounds or agents, either in vitro or in vivo.

E20= Mechanisms: The report defines, or is in some way related to, the molecular mechanism(s) of action of the compound.

E30= Kinetics: Related to the pharmacodynamics of a toxic compound or an agent used in treatment.

E40= Treatment: The document reports the effectiveness of one or more therapeutic agents in treating a toxicosis induced by an agent.

E50= Pharmacol: Involves drugs; their actions, toxicity, and effectiveness.

E60= Chemistry: The document is primarily one which is associated with the chemistry of a compound. This category is further broken down into the following:

E61= Analysis: Includes detection, and new methods of detection.

E62= Synthesis: Includes the synthesis of radiolabeled compounds, metabolites and congeners.

E63= Purific.: Deals with the purification of a compound involving new methods of isolation, improved yields, etc.

N10= Case Report: (described above)

N20= Epidemiology: (described above)

I01= Review: (described above)

I02= Comment: (described above)

C01= Case+Review: (described above)

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PAPER OVERVIEW SCREEN: Number of Study Designs in Paper

This may be simply stated in the manuscript, but more often you will have to carefully check the material and methods section (and sometimes the Results and Discussion) to determine the number of designs used in the experiments described. Usually there will be a single study design for each particular question or hypothesis.

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Defining the study design goes hand in hand with determining the questions being asked. Good researchers will specifically state their hypotheses and this, in turn, will help you in entering their paper into the database.

You may use the arrow keys or the "return" key to cycle through portions of this screen if the need arises. You might think of a better way to express the implied purpose, or you may have made an error that needs to be corrected.

Remember, useful keys for correcting misspellings are the "Control-x" sequence to erase a letter in an entry, and "Control-a" to insert characters.

Enter the number of designs and hit "Esc," since you are done with this screen. The STUDY DESIGN DATA SCREEN comes up next.

.404

Paper Overview Browse: Delete

Selecting this option will bring up the question "Do you want to delete this paper overview? (y/n)" Type in the appropriate letter and hit "return."

.405

THERE ARE MORE DESIGNS THAN INDICATED: Cancel

In the PAPER OVERVIEW SCREEN there is a field for indicating the number of designs described in this paper. If you attempt to "Add" paper overview data to a citation which already has it you will be given the opportunity to "Update" that data. You can also "Update" that information by following the "Find" path and choosing the "Update" option from the BROWSE menu.

If you update the number of designs to a lower number, the system recognizes that either an error was made in entering the new number, or design data needs to be deleted from the records.

"Cancel" is the option which provides a means to go back to the overview screen and change the number of designs if an error was made during the update.

.406

THERE ARE MORE DESIGNS THAN INDICATED: Delete Design

In the PAPER OVERVIEW SCREEN there is a field for indicating the number of designs described in this paper. If you attempt to "Add" paper overview data to a citation which already has it, you will be given the opportunity to "Update" that data. You can also "Update" that information by following the "Find" path and choosing the "Update" option from the Browse menu.

If you update the number of designs to a lower number, the system recognizes that either an error was made in entering the new number, or design data needs to be deleted from the records.

"Delete-Design" provides a mechanism to search for and delete the designs you wish to remove.

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DELETE_PAPER: Paper-Only

Using this option you will delete ONLY the Paper Overview portion of this citation abstract, NOT other data tables linked to it such as designs, subject information, regimens, etc.

You can correct information in the PAPER OVERVIEW SCREEN by doing an "Update," which can be accessed via "find"ing the citation and choosing "Update" from the BROWSE menu.

.408

DELETE_PAPER: All Links

In choosing this option, you will delete not only the information in the PAPER OVERVIEW SCREEN, but also all the data tables linked to it, such as designs, subject information, regimens, clinical findings, etc.

.409

DELETE_PAPER: DO YOOU REALLY WANT TO DELETE ALL CONNECTED TABLES?

(No)

This is a safeguard against accidentally removing data that someone worked hard to place in the database.

Using this option, which has such broad deletion powers, suggests that there are major problems with the data as entered. The most efficient approach to correcting them is to delete nearly all of the data and start over.

Type "n" followed by "return," if you do not wish to delete all of the tables. Type "y" followed by "return," if you do.

.410

DELETE_PAPER: DO YOOU REALLY WANT TO DELETE ALL CONNECTED TABLES?

(Yes)

This is a safeguard against accidentally removing data that someone worked hard to place in the database.

Using this option, which has such broad deletion powers, suggests that there are major problems with the data as entered. The most efficient approach to correcting them is to delete nearly all of the data and start over.

Type "n" followed by "return," if you do not wish to delete all of the tables. Type "y" followed by "return," if you do.

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Which of the design should be deleted?

Below this statement on the data screen are one or more lines representing the design number (left margin), the number of subject groups and regimens in that design, and whether or not control groups were included.

If the numbers are not sufficiently descriptive, you need to go to the "Find" option in the ABSTRACT menu and follow the path to find the design you wish to delete. This method will allow you to directly visualize the data in the design (and potentially the other data tables linked to it). A BROWSE menu is available when a data table is found, and "Delete" is an option in that

menu.

You can abort this process, even at this late stage, by using the "delete" key as your response.

.-1 tkdsgr.4gl Help Messages

.500

STUDY DESIGN DATA SCREEN: Type of Study

Enter a selection from the menu to the right by typing the corresponding abbreviation followed by "return."

Note: You can move through the different fields in this screen by using the arrow and/or return keys. This is particularly useful if you find that an error has been made and you need to edit a previous field.

The type of selection screen which comes up after an entry depends on the response in a previous field. For example, if you indicated earlier in the OVERVIEW screen that the paper being entered was an "Info only" paper, then you wouldn't have been able to indicate there were study designs, since those sorts of papers do not generally include experiments (experiments should have designs).

With the current screen, if you do indicate that there are no controls, you won't be able to enter the fields from "comparison Info" on down.

{Do we want to enter stycitfile, dsgncur, dsgntot, dsgncw, dsgntr? (y/n)}

.501

STUDY DESIGN DATA SCREEN: In Vivo or In Vitro

Again, select from the menu to the right and type in the appropriate classification, followed by a "return."

.503

STUDY DESIGN DATA SCREEN: Controls (y/n)

Enter "y" if negative controls were used in the experimental design and "n" if they were not (followed by "return").

.504

STUDY DESIGN DATA SCREEN: Comparison Info

If the answer to the above is "y," then you will be able to enter information in this and following fields. Type the correct letter from the pop-up menu and hit "return."

.505

STUDY DESIGN DATA SCREEN: Comparison Methods

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Type the appropriate letter and number followed by "return."

.506

STUDY DESIGN DATA SCREEN: Control Methods

Type the proper letter (no return necessary).

.507

STUDY DESIGN DATA SCREEN: Control Types

Type the correct letter and then "return."

.508

STUDY DESIGN DATA SCREEN: How were subjects assigned to their groups?

Type the appropriate letter followed by a "return."

.509

STUDY DESIGN DATA SCREEN: Number of Subject Groups

Examination of the report is necessary to determine the appropriate response here. Please note that the number of subject groups encompassing the current design should be entered here (not the total number of subject groups for the entire report)! Enter the number followed by "return." This brings up the first "SUBJECT GROUP DATA SCREEN." It will be followed by additional similar screens if you indicated that there are multiple subject groups. Hit "return" to automatically enter the Citation No. and move the cursor to the first data field.

.510

STUDY DESIGN DATA SCREEN: Number of Exposure Regimens

An exposure regimen encompasses the different types of treatments that have been given. For example, giving a different dose or a longer exposure would constitute a different regimen. Enter the number followed by "return."

.511

BROWSE: Delete this entry from database

The delete option provides different capabilities for different components of the TKS system. The "design" delete function allows deletion of the design screen shown on-screen, as well as all "tables" linked to that design.

.512

BROWSE: Query-Again

If you would like to perform another search this option will allow immediate access to the screen for entry of another search parameter without having to "Exit" all the way back to the "Find" option in the ABSTRACT menu.

You may search for any single entry (such as the citation number or type of study), or use several fields of interest (e.g., Type of Study and In Vivo) to further narrow down the potential matches. In addition, wild cards (*) can be used to help compensate for some differences in terminology.

.513

DELETE-DESIGN: Design Only

Selecting "Design Only" will cause only the design shown on-screen

to be deleted. The remaining "Links" such as the subjects and regimens will be left intact. If one wishes to delete all associated links along with the current design, choose the option "All Links."

.514

DELETE-DESIGN: All Links

If you choose "All Links," the current design, as well as all subjects and regimens linked to it will be deleted. If you only want to delete the current design (the one shown on screen), use the option "Delete Only."

.515

DELETE-DESIGN: ARE YOU REALLY SURE..... (No)

.516

DELETE-DESIGN: ARE YOU REALLY SURE..... (Yes)

.-1

tkssgro.4gl HELP MESSAGES

.600

SUBJECT GROUP DATA SCREEN: Group [] of [] of design [].

The screen indicates which group of the design you will entering, the total number of groups, and which particular design.

The designation for the first group (they are assigned sequential numbers) comes up automatically. Hit "return" to go to the "Source" field. If you would like to enter subject data for some other group, enter its number designation followed by "return."

The next two fields are bracketed differently than the others. You cannot change them because they were derived from the design screen. Therefore, a "return" after "Group" brings the cursor to the "Species" field where the common name of the animal used can be entered. Another "return" places the cursor in the "Breed" field.

.601

SUBJECT GROUP DATA SCREEN: Exposure Group

Note that to the right of this heading and the subsequent fields is a statement ExpoGrp < > of < >.

These two fields will be filled in and the system usually begins with exposure group 1 of however many groups there are.

The designation for the first group (they are assigned sequential numbers) comes up automatically. If you would like to enter subject data for some other group enter its number designation followed by "return."

Note that the next two fields are bracketed differently than the others. You cannot change those fields in this screen because they were derived from the design screen.

Toxin Knowledge System Source Code

Therefore, a return after "Group" brings the cursor to the "Species" field where the common name of the animal used can be entered. "Return"s move you through the screen.

.602

SUBJECT GROUP DATA SCREEN: Source

The "Source" field is meant to be used to identify where the animals came from.

.603

SUBJECT GROUP DATA SCREEN: Number

"Number" refers to the number of animals in the group.

.604

SUBJECT GROUP DATA SCREEN: Sex

The following are suggested abbreviations for "Sex:" F for female; S for a neutered female; P for a pregnant animal; L for a lactating one; M for male; C for a castrated male; and B for both male and female. The program converts lower case letters to upper case so there is no need to use the shift key. There are four spaces in the field so it is possible to use some combinations. If all four spaces are filled, the cursor jumps to the next field.

.605

SUBJECT GROUP DATA SCREEN: Age

Animal age can be represented in any form using numbers in the first field and units of time in the second (when the cursor is in the second field a note at the bottom of the screen requests that units be entered).

We recommend that the age of the subject at the time of study initiation be placed in this field. Since the duration of the study is given in the EXPOSURE REGIMEN DATA SCREEN, the user can calculate the age of the subject at the time of evaluation if it is not specifically given.

.606

SUBJECT GROUP DATA SCREEN: Weight

Subject weights may be entered in any form. Usually they will conform to the article format. The first field is for a number and the second for the units (as indicated by the message at the bottom of the screen when the cursor is in the second field). Metric units are preferred, and in fact, the program converts all entries to a metric format.

The question arises, "what do you enter, a range of weights or a mean, or individual weights?" Currently, there is no provision for providing either individual weights when more than one animal is used, or a range of values. Provide the mean, or an estimate of it.

.607

SUBJECT GROUP DATA SCREEN: Height

As for the above, the first field should be a number and the second a unit of measure. Suggested abbreviations are indicated.

.608

SUBJECT GROUP DATA SCREEN: Occupation

Papers involving people will often provide their occupations.
There are twenty spaces available for this entry.

.609

SUBJECT GROUP DATA SCREEN: Health Status of Subjects

If this is not reported in the publication, leave the space blank, or indicate that no information is available (type in "UNKNOWN"). If it is, try to indicate the status in the space provided or type a more lengthy comment in the comment section and indicate in this field. (THE COMMENT SECTION IS NOT YET READY FOR USE.)

.610

SUBJECT GROUP DATA SCREEN: Number of Exposures Received

This field can provide more information than just whether there was a single or multiple exposure. What frequently arises is "What about constant exposure to diet?" We suggest that this be handled by typing "INDIET" in the spaces provided. Again, special remarks can be made in the comment section.

When the first subject screen is completed, typing return after the last entry will cause the next subject screen to come up. This is indicated by the "Group < >" designation. You can go back and forth between subject screens by using the up and down arrow keys.

.611

BROWSE: Delete this entry from the database

Selecting "Delete" from the BROWSE menu will result in the removal of the current subject group from the citation, and the database.

.612

BROWSE: Query-Again**TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Query-Again**

If you would like to perform another search this option will allow immediate access to the screen for entry of another search parameter without having to "Exit" out all the way back to the "Find" option in the ABSTRACT window.

You may search for any single entry (such as Rat in the species field), or use several fields of interest (RAT, SPRAGUE-DAWLEY, FEMALE) to further narrow down the potential matches. In addition, wild cards (*) can be used to help compensate for some differences in terminology.

-1

R. Want to add statements for citfile, grp [] of [], etc?
see tkssubgrp.per

..1 tksexgrp.4gl HELP MESSAGES

.700

EXPOSURE REGIMEN DATA SCREEN (Overview)

A "return" will fill in the "Citation No." field. Again, you can identify where you are by looking at the description under "Citation No." which tells you how many regimens there are (based on what you typed in previously) and which one you are currently describing. As before, fill in the appropriate data by selecting from the options available at each field. You do not need to fill in every field, only those which are defined in the report. For example, if you indicate that there was only one exposure, then you need not fill in the field "every."

There is no set format for filling in these spaces, try to make the information as descriptive as possible. Filling in the entire field causes the cursor to roll over to the next one. If you do not entirely fill in a field, you must hit "return" to move to the next one.

When you fill in the last field, and assuming there are multiple regimens, the next screen is brought up with the cursor on the "Citation No." field. Hit "return" to fill it in. Once again, the up and down arrow keys enable you to move between the regimen descriptions.

When the regimen screen(s) is/are completed, the next design screen comes up and the cycle begins again. Please note that "return" will fill in the "Citation No." Hit "return" when the cursor moves to the "Group" field.

When all of the design, subject and regimen screens are complete, you can establish the proper links between them. This means placing them within the proper relationships so that, for example, the design for the rabbit portion of the study is properly related to the rabbit subject group and exposure regimen.

.701

EXPOSURE REGIMEN DATA SCREEN: Purpose for Exposure

This field is used for defining the reason for administering (or not administering, in the case of some control groups) the agent. Was it an effort to define some aspect of toxicity or evaluate a therapy? Determine pharmacodynamic characteristics such as plasma disappearance or metabolism (Other)?

.702

EXPOSURE REGIMEN DATA SCREEN: Agent

Enter the name, or a brief description of the agent described in the document. If it is unknown, you could use a description of the presumed agents' action such as "hepatotoxic agent" or "hemolytic agent."

.703

EXPOSURE REGIMEN DATA SCREEN: Dose

Dose refers to the quantity of the agent administered within a given period. Provide the amount and the units of measure.

With airborne exposures to gases and particulates, it is generally not possible to define the dose administered. Instead, the characteristics of the gas or particles, and the concentration, in conjunction with the duration of exposure, and sometimes the rate of breathing and tidal volume, are used to define the exposure.

.704

EXPOSURE REGIMEN DATA SCREEN: Formulation

Insert the numbers from the options provided to the right, in the space provided.

The options should be largely self explanatory. "Slo_rel" is slow release formulation. "Concent" means concentrate, not concentration. A concentrate is a formulation which is added to a mix which dilutes it out.

.705

EXPOSURE REGIMEN DATA SCREEN: Route

Select the route of administration of the agent from the list provided. The abbreviations should be self-explanatory with the possible exceptions of IA and Bite-St. IA means intra-arterial and St means sting.

.706

EXPOSURE REGIMEN DATA SCREEN: Interval

This and the following field are designed to provide the user with a way to define multiple dosing protocols. If an agent is given every hour, q. 1h would define the interval. The q. is an abbreviation for "quaque" which is latin for "every." It can be used with minutes, hours or days. Everything typed in the Interval field is converted to upper case, so a "q" will be represented by "Q."

Currently, there is no direct mechanism for indicating unequal intervals in the EXPOSURE REGIMEN DATA SCREEN. The comment section could be used for this purpose.

.707

EXPOSURE REGIMEN DATA SCREEN: Duration

This field is to be used for indicating the length of time over which the agent was given. In the case of an IV injection it may be five seconds or 50 minutes, whereas an orally administered compound may be given every 12 hours for six months.

There are no predefined limits on how the information can be represented. The goal is to be as descriptive as possible.

.708

EXPOSURE REGIMEN DATA SCREEN: Administration Method

Indicate the method of giving the agent. The methods are numerous and there is enough space to include a brief description. Was it administered orally via a balling gun, IV via a Harvard infusion pump or as an aerosol by a Lovelace nebulizer? Was it a syringe/needle injection or dietary consumption?

.709

EXPOSURE REGIMEN DATA SCREEN: Scheduled Evaluation Time?

When will blood samples be taken or the animal killed for tissue collection? There may not be room to define some multiple evaluation schedules. Abbreviations that aren't cryptic help, e.g. 2, 4, 6, 12, 24H & 2, 4, 7D (the spaces can be removed to offer more flexibility).

-1 tksexpgrp.4gl HELP MESSAGES

.800

EXPOSURE GROUP LINK ENTRY SCREEN: (Overview)

The EXPOSURE GROUP LINK ENTRY SCREEN provides a means of storing the association of design, subject group, and exposure regimen with the subsequent results. This screen allows the user to form the associations, which then constitute an "Exposure Group." This process creates and stores a derived number and brief descriptions of the design, subject group, and exposure regimen for the "Exposure Group."

Hit "s" or "return" to see the Help for "Citation No."

EXPOSURE GROUP LINK ENTRY SCREEN: Citation No.

The "Citation No." can be filled in using "return" unless you are performing a search.

.801

EXPOSURE GROUP LINK ENTRY SCREEN: Exposure Group (first field)

"Exposure Group" is not asking you to give a number or letter for an exposure group per se. Rather, the first field is for indicating the design for which you are setting up links. The designs are listed and numbered in the middle of the screen. Use the number to the left of the "=" sign to designate the "Dsgn" choice.

Entering a valid design number (followed by "return") will cause the conditions you entered earlier for that design to pop up: (in abbreviated form) next to "Dsgn" in the upper portion of the screen. Also note that an abbreviated form of each subject description appears mid-screen.

.802

EXPOSURE GROUP LINK ENTRY SCREEN: Exposure Group (second field)

The cursor is now at the second field where the number for the subject portion of the link can be entered. Select one of the numbers to the right of "Subj:"

Completing that field results in your selection appearing to the right of the "Subj:" heading below. The choices of regimens described previously are now in the middle of the screen, and the cursor is on the "regimen" field.

.803

EXPOSURE GROUP LINK ENTRY SCREEN: Exposure Group (third field)

Select the correct regimen number from those appear to the left

of the "=" sign. Completing this field causes the final field in the "Exposure Group" row to show the abbreviations of the previous three fields with the number of the design (D), subject (S) and regimen (R) linked.

.804

EXPOSURE GROUP LINK ENTRY SCREEN: ExpoGrp (second field)

The cursor is now on the last field of "ExpoGrp < > of < >."

This number should match the number of total exposure groups for the design. If the number is incorrect, enter the correct number, followed by "return."

Hit "return" until the fields clear (and the citation number is filled in) and the cursor is on the first field to the right of "Exposure Group" as above.

The process now begins again for the next subject group for the first design. Repeat the steps as described above.

When the first design is complete, and the cursor is on the first field to the right of "Exposure Group," enter 2 for the second design number and repeat the entry steps until all associations are entered for each design, exposure group and regimen.

.805

BROWSE: Delete this entry from database

Select this option when you wish to remove the Link data.

.806

BROWSE: Query-Again

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Query-Again

If you would like to perform another search this option will allow immediate access to the screen for entry of another search parameter without having to exit out all the way back to the "Find" option in the ABSTRACT menu.

You may perform a search using any single entry, or several fields of interest, which will narrow down the potential matches. In addition, wild cards (*) can be used to help compensate for some differences in terminology.

.-1 tksvoc.4gl HELP messages

.900

TKS-MAIN VOCABULARY JOURNAL-VOCABULARY: Add

Selecting "Add," puts the cursor on the "Journal Name" field of the JOURNADD DATA SCREEN. Type in the journal name as given in the National Library of Medicine List of Journals Index. Hit "return" until the "Journal Abbreviation" field is reached and enter the appropriate abbreviation as given by that Index. Hit "Esc" and the journal is assigned a Journal Code Number. The numbers are unique to each journal, and assigned sequentially.

.901

TKS-MAIN VOCABULARY JOURNAL-VOCABULARY: Find

Selecting "Find", puts the cursor in the "Journal Code" field of the JOURNADD DATA SCREEN. More commonly you will need to use the "Journal Name" field, so hit "return" to place the cursor there and type in the EXACT name of the journal (see below). Hit "Esc," in order to find its journal code.

If you typed the name correctly and it is already in the system, the remaining information for that entry is now provided on screen. If there is no match, check your spelling and title. If they are correct, and there is no match, you will have to enter it as a new journal via the "Add" feature. Go back to the JOURNAL-VOCABULARY screen and follow the "Add" path.

You do not have to type in the whole name of the journal, you can use the first few letters of the first word or the first word or two and a "wild card" symbol (*). For example, type in "American*" and hit "Esc." The message at the bottom left corner of the screen tells you how many matches were found. Increasing the length of the search pattern will decrease the number of matches you obtain.

You can now "cycle" through the matches by using the first four options indicated in the BROWSE menu near the top of the screen.

.903

TKS-MAIN VOCABULARY KEYWORD_LISTING: Add

The ADDKEYS DATA SCREEN provides a mechanism for adding keywords to the system list of keywords, and assigning them a keycode.

.904

TKS-MAIN VOCABULARY KEYWORD_LISTING: Find

This option provides a mechanism for locating keywords and their associated keycodes.

.906

TKS-MAIN VOCABULARY BOOK-VOCABULARY: Add

Selecting "Find," puts the cursor in the "Book Code" field of the BOOKADD DATA SCREEN. Fill in the title and other fields and hit "Esc." The book is assigned an "Acquisition" and Code" number and is entered into the system.

.907

TKS-MAIN VOCABULARY BOOK-VOCABULARY: Find

Selecting "Find," puts the cursor in the "Book Code" field of the BOOKFIND DATA SCREEN. More commonly you will need to use the "Book Title" field, so hit "return" to place the cursor there and type in the EXACT title (see below). Hit "Esc," in order to perform the search. You can, of course, use any or all of the other descriptive fields in the search process if you wish.

If you typed the title correctly and it is already in the system, the remaining information for that entry is now provided on screen. If there is no match, check your spelling and title. If they are correct, and there is no match, you will have to enter it as a new book via the "Add" feature. Go back to the BOOK-VOCABULARY menu and follow the "Add" path.

.908

BROWSE: Delete (Journal)

Selecting this option will enable you to delete the current on-screen journal from the master system list. Once selected, there is one more query to which you must respond before the journal is deleted from the list.

BROWSE: Delete - Are you sure you want to delete this Journal? (y/n)

Typing a "y" will delete the indicated journal from the master system list. Typing "n" will return you to the BROWSE menu.

.909

BROWSE: Delete (Book)

Selecting this option will enable you to delete the current on-screen book from the master system list. Once selected, there is one more query to which you must respond before the book is deleted from the list.

.910

BROWSE: Delete (Keyword)

Selecting this option will enable you to delete the current on-screen keyword from the master system list. Once selected, there is one more query to which you must respond before the keyword is deleted from the list.

-1 tksvoc2.4gl HELP messages

.911

SIGN-VOCABULARY: Add

You can add new signs to the vocabulary list by selecting "Add."

This function is not yet implemented.

.912

SIGN-VOCABULARY: Find

This function is not yet implemented.

.913

SIGN-VOCABULARY: Site

This function is not yet implemented.

.914

SIGN-VOCABULARY: Rest

This function is not yet implemented.

.915

BROWSE: Delete

-1 tkstinding 4gl HELP messages

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.1001

CLINICAL-FINDINGS: OneSign->ManyGroups

.1002

CLINICAL-FINDINGS: ManySigns,-One-Group

.1003

BROWSE: Delete

.1004

BROWSE: Query-Again

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Query-Again

.1005

EFFECTS SEARCH-ALL: FirstWord

.1006

EFFECTS SEARCH-ALL: AnyWord

.1007

EFFECTS: All

.1008

EFFECTS: Morph

.1009

EFFECTS: Funct

.1010

EFFECTS: Disease

.1011

EFFECTS: Procd

-1

tksbrowse 4gl HELP messages

.1100

BROWSE: Delete

.1101

BROWSE: Delete

-1

tksmonogrp1 4gl HELP messages

.1200

SELECT FILE-BY Author-Name

.1201

284

SELECT-FILE-BY: Citation-Number

-1 tksquery.4gl HELP messages

.1300
BROWSE: Output

.1301
OUTPUT: Printer

.1302
OUTPUT OUT-TO-PRINTER: This-Citation

.1303
OUTPUT OUT-TO-PRINTER: All-Citations

.1304
OUTPUT: File

.1305
OUTPUT OUT-TO-FILE: This Citation

.1306
OUTPUT OUT-TO-FILE FILE-SELECTION: New File

.1307
OUTPUT OUT-TO-FILE FILE-SELECTION: Append-To_File

.1308
OUTPUT OUT-TO-FILE: All-Citations

.1309
OUTPUT OUT-TO-FILE FILE-SELECTION: New-File

.1310
OUTPUT OUT-TO-FILE FILE-SELECTION: Append-To-File

-1 tksshows.4gl HELP messages

.1400
CURRENT-CITATIONS: Next

.1401
CURRENT-CITATIONS: Previous

.1402
CURRENT-CITATIONS: Select

.1403
CURRENT-CITATIONS: Use-Current

.1404
CURRENT-CITATIONS: Next

Toxin Knowledge System Source Code

.1405

CURRENT CITATIONS: Previous

.1406

CURRENT-CITATIONS: Select

.1407

CURRENT-CITATIONS: Use-Current

.1408

CURRENT PAPER: EXIT

-1

Rich's PLAYGROUND

-.0000

Clinical "Findings" is another citation component which can be "searched" from the Browse menu in the Find- pathway. One can search for certain clinical findings or search for a citation and obtain the clinical findings associated with it.

Design

Subjects

Regimens

Links

Delete

Findings

The process of finding these particular portions of the abstract is similar to that described above for Paper Overview. One should be aware that you will frequently encounter multiple matches for such things as Subjects, Regimens and Links, since many experimental studies have several of those components. You can switch back and forth between those multiple screens by using the up and down arrow keys. Note that multiple matches may include components from several citations, especially if wild cards (*) are used. Check the Citation No. as the screens change in order to be aware of where you are.

Some screens require that you re-enter data for certain fields in order to cycle through the entire screen. Query-Again is an option in the Browse menu for Design. Deleting a design gives you the option to delete only the design on screen, or the design screen and all of the screens from that point forward (Subjects, Regimens, Links, etc.). The same is true of "Delete" and the other citation components; you can either delete the data on that screen alone, or that screen and all screens linked to it in the forward direction.

-1001

Subject

The subject screen comes up with the cursor on the "citation No" field. Hit "return" which fills in that field automatically and moves the cursor to the next one. The designation for the first group (they are assigned sequential letters) comes up automatically. If you would like to enter subject data for some other group enter its letter designation followed by "return."

Note that the next two fields are bracketed differently than the others. You cannot change those entries in this screen because they were derived from the design screen. Therefore, a return after "Group" brings the cursor to the "Species" field where the common name of the animal used can be entered. "Petum"s move you through the screen. "Source" is meant to be used to identify where the animals came from. "Number" refers to the number of animals in the group.

This goes with the "New Citation" path helps.

Add-Design

A "Return" causes the screen to come up with the Citation Number (No) and File Number sections filled in. Type "return" until the first empty field is reached and then begin filling in the appropriate responses. The possible options are listed as the cursor moves to each new field. When all the data for that screen has been entered, hit "Esc" and the next design screen will come up as indicated by the different "Design No." If the "citation Numb" (No) is not present, hit "return" and it will appear.

option I

When all the design screens have been completed, hit "Esc" followed by "E" until you reach the menu with the "Add" option. Select "Add", and then the "Subject" option from the "FIND-CONTENT" menu.

option II

If the subsequent Subject sections have not been completed, the program will bring you to that section to provide the necessary information. The entry process is similar to that described above under the appropriate screen heading.

..1 ...This section must be moved to the tksauth.4gl module.....

Last name, first author

Enter the author information (lower case letters are acceptable), then hit the "return" key.

..1 We need to move the following section.

SELECT-FILE-BY

Toxin Knowledge System Source Code

From here, one can search for a specific citation by responding to sequential screens which request the Author, the journal volume number, the first page number, and last two digits of the year. Alternatively, one can give the Citation No. which consists of the source code of the journal or book, the volume number, first page number, and the year. Note that for the latter, each component must consist of a certain number of characters, for example, J00001-0001-00001-1988.

xxxxxxxxxxxx

Completion of the process will result in finding the desired citation, or a message that the citation doesn't exist in the database. If a citation isn't in the system, you can't add anything to it. Enter a new citation by starting from "New" in the "ABSTRACT" screen.

.-1 The following needs to be moved so it is available when the Browse menu is on screen.

Browse

Using the "Browse" options, one can choose to: view the next citation if more than one match is found in a search; see the previous citation if the "Next" or "Last" options were used; go to the "Last" citation in the list of more than one match (the matches are arranged chronologically in the order in which they were entered into the system); "Update": (modify or change) an entry; "Delete" the entry shown on-screen (with the option of deleting other portions of the data, e.g. Paper Overview, Design, etc.); "Query-Again" which clears the data fields and allows one to search for another citation; or "Exit" from the program.

xxxxxxxxxxxx

Not all of the options are evident at one time. To see the others, use the right and left (horizontal) arrow keys to move among the selections and see those on the right after the "...." notation. When the first option is highlighted (Next) you can use the left arrow key to see the end of the option list (horizontal wrap around for the Browse option list).

.-1....The following section needs to be moved to PaperOverview.....

.?

PaperOverview

When this option is selected, a replica of the Overview screen comes up with the cursor on the Citation No field and a statement: "Enter search criteria and hit ESC to search." One can search via any of the fields represented on the screen, but the Citation No and File fields will be most commonly used.

.24

Update

Selecting "Update" places the cursor on the Source field. You can cycle through the data fields by using the "return" key which functions in only one direction, or the left and right arrow keys. Change the appropriate field and hit "Esc" when you are finished. Wait for the cursor to return to a data field or menu. This procedure writes the updated information to memory.

.-1

VOCABULARY-Keywords

"Selection of this option brings up the "KEYWORD_LISTING" screen from which one can add new keywords and keycodes, or find existing ones. Once found, they can be modified.

xxxxxxxx

.-1

VOCABULARY-Signs

This option is used to add clinical signs to the Sign Vocabulary list, find a sign which is already in the system (after which it can be modified), obtain site information (system programmer use), and access the SNOMED listings.

xxxxxxxx

.24

Update

Selecting "Update" places the cursor on the Source field. You can cycle through the data fields by using the "return" key which functions in only one direction, or the left and right arrow keys. Change the appropriate field and hit "Esc" when you are finished. Wait for the cursor to return to a data field or menu. This procedure writes the updated information to memory.

1

.123

Citation-File No.

Typing "return" again, fills in the "File No" field automatically. It consists of the first four letters of the first author's last name, the journal or chapter number, the beginning page number and last two digits of the year. This number may also be used to find the file after it is entered into the system. It does not consist of extra characters or spaces. There are periods separating portions of the entry (e.g. SMIT.10.23.1988).

xxxxxx

Hit "return" again. If the citation you are attempting to enter is already in the system, you will receive notification of that fact. You may make changes in a file that is already in the system, but not from the "New" citation pathway. "Exit" back to the "ABSTRACT" window and begin the entry process again for a new article.

xxxxxxxx

If the citation is not in the system, hit "return" to move to the title entry field.

xxxxxx

.....Below is indeed a copy of part of .123 which should be available after the message indicating that "information for that citation has already been entered" pops up...I think it goes with the tksshow.4gl file about line 483 because the next place where help would be useable is the Current-Citations (all caps) screen.

xxxxxx

tksshow.4gl

.124

Duplicate citation

Hit "return" again. If the citation you are attempting to enter is already in the system, you will receive notification of that fact. You may make changes in a file that is already in the system, but not from the "New" citation

Toxin Knowledge System Source Code

pathway. Exit back to the "ABSTRACT" window and begin the entry process again for a new article.

xxxxxxx

.-1 The following goes with the Find path, to the citation and update. It is a "browse" path (update) but the author list portion is in tksauth.4gl, hence the .201 number.

xxxxxxxxx

.201

Find-Update

The "Author" screen comes up next. Hit "Esc" as indicated at the bottom of the screen. The program will ask if you want to update the author list. If you select "n" the keyword list comes up.

Selecting "y" places the cursor on the first data field.

xxxxxxxxx

Change it if necessary, or use the arrow or return keys to cycle through the fields. Modify the entries or type in new authors, and then hit "Esc." The file is updated and the Keycode/keyword screen comes up.

xxxxxxxxx

.203 This should probably be done away with....I'll wait to be sure.

Authors

The author screen can be updated directly as well as indirectly as just described above. Selecting Author from the FIND-CITATION-DATA screen brings up the author screen with the cursor on the citation number field. Enter the citation number and then "Esc." The screen comes up with a message in the lower left corner indicating how many matches were found and asks you to "Esc" to continue. A Browse menu appears with options similar to those described above under "citation."

xxxxxxxxx

.-1 This following paragraph is meant to come up when following the New citation-path. after the title and authors, one is asked to insert keywords. Then, 300 should be available.

The "Find" option helps you search for particular keywords that are in the list, and identifies their associated keycode.

xxxxxxxxx

Type "F" and the cursor is placed on the first field (keycode). Hit "return" and the cursor goes to the next field. Type in the word "mouse" and hit "Esc." The program searches for that keyword and, if it is found, fills in the keycode number. One can complete those two fields for the paper being abstracted by hitting "Esc" once again. From there the process starts over again for the next keyword. If a keyword is searched for but not found, the program returns the message that "There is no keyword matching the first three letters" and returns you to the original screen.

xxxxxxxxx

.xxx

The "keyword" screen appears next, and the same process occurs again. Refer to the section on keywords for information on this screen. When you are finished modifying this screen hit "Esc." This completes the process of "Update" for citations. You are returned to

the citation screen with the Browse menu. Hit "e" to exit from this environment and return to the FIND-CITATION-DATA screen.

.302

The "Add" option allows the freedom to place new keywords and their accompanying codes into the list. If you do not wish to enter keywords at this time, hit the "delete" key. If you follow this later path, the screen indicates that it is preparing citation "information."

xxxxxxxxxx

The next screen is titled "current paper" and has only one option, "Exit." That is because you are finished with the first part of the system and must begin a new phase of data entry for the citation. Hit "E" or "return" to go on. You are then asked if you would like to "add content data for the paper?".

xxxxxxxxxx

If you type "n" then "return", the system goes back to the "Abstract" screen. Typing "y" followed by "return" results in a new screen which begins the paper overview process.

.404

Enter the Citation No for the paper you wish to find and then "Esc." The program will search and then tell you how many matches were found and a Browse menu will appear. The Browse options are explained under Find-Citation, above. There is no Query-Again option, but there is an Add-Data option which allows one to add a component (Design, Subject group etc.) if none is found during a search. If no match is found, you will still get a Browse menu, and can try again by exiting from the screen ("e") and reselecting Paper Overview, or return to try another path or option.

Old help .64

Authors may be added to the list generated when the citation was first entered into the system. Select "Authors" and respond to the prompts.

Old—— tksauth.4gl HELP MESSAGES

.A

TKS-MAIN ABSTRACT SELECT-FILE-BY ADD-DATA ADD-CITATION-DATA: Authors

As the menus suggest, one can add authors to a partially completed list or add authors to a citation that lacks that feature.

If there are authors already listed for the citation, you can move through them with the cursor keys. You cannot change anything or add names until the "Esc" key is used.

After hitting "Esc" the message at the bottom of the screen

Toxin Knowledge System Source Code

changes and the cursor field is in reverse video (dependant on your terminal type). You can now make changes in the fields already entered or add names to the list. Remember, the program will correctly number the authors if you enter them in sequence.

When you are finished with the changes/additions, hit "Esc" to place them in the system memory.

.B

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA: Authors

This screen comes up with the cursor on the Citation No. You have indicated that you would like to find an author so you probably don't want to institute the search process based on that number. Move through the fields using the "return" or cursor keys until the cursor is in the first author field. Type in the name of the author (including initials!) whose citations you wish to locate, and hit "Esc" to initiate the search process.

You can search for all "Smith's" regardless of their initials, by using the wild card (*), e.g., "SMITH*."

It may be preferable to use the wild card in place of both initials because some journal articles may not provide the names with both initials. Some people may not choose to enter both initials. Some people may ignore the plea to NOT place spaces between the initials, which means an exact match would need to have both initials matched as well as the spacing!

A search using the first initial and a wild card will pick up all the single and double initials, regardless of the spacing. However, be aware that you must pay attention to the initials in order to weed out any matches that aren't exactly the author of interest.

If a match is found, a BROWSE screen appears which provides you with several options.

.-2000

CITATION DATA SCREEN: New-Source - Not a Journal or Book!

This message commonly occurs when the "J" or "B" prefix has not been used.

.-11000

CITATION DATA SCREEN: Year - Not a valid year!

You need to type in all four digits of the year or correct a typing error.

Old tksauth help messages

.C use help .170

BROWSE: Next (Author)

The BROWSE menu appears as a result of a search process. It provides mechanisms for moving between components when more than one is found (Next, Previous, First and Last) a method for changing entries (Update), removing components (Delete), performing another search process (Query-Again) and exiting from the BROWSE menu (Exit).

.D use help .171

BROWSE: Update (Authors)

The "Update" option provides a means for changing any author component in a window and, hence, the database entry. This is necessary when a component has been incorrectly or incompletely entered.

"Update" allows you to add or delete authors. To add authors to the end of a list, scroll through it using the down arrow key until an empty author field is reached. Then, type in the name of the author followed by an "Esc."

If an author needs to be placed in the middle of a list, place the cursor on the line below where you would like the name added and hit the "F1" key. A new line will be opened and you can type in the name followed by an "Esc," which will write it to memory and change the numbering sequence.

To delete authors you must place the cursor on the line you would like to delete and hit the "F2" key. The line will be deleted, and after an "Esc," the numbering sequence will be corrected.

.F

BROWSE: Query-Again

If a search is uneventful, or if one would like to perform another one, this option will allow immediate access to the screen for entry of another number.

Old tkskey helps

.C use .170 as help

BROWSE: Next (Keyword)

The BROWSE menu appears as a result of a search process. It provides mechanisms for moving between components when more than one is found (Next, Previous, First and Last) a method for changing entries (Update), removing components (Delete), performing another search process (Query-Again) and exiting from the BROWSE menu (Exit).

.D use .171 as help

BROWSE: Update (Keyword)

The "Update" option provides a means for adding, modifying or deleting keywords. When it is chosen, the cursor goes to the "Citation" field. Use the arrow or "return" keys to place the cursor on the desired keycode line.

To add keywords to the end of a list, scroll through it using the down arrow key until an empty keycode field is reached. Then, type in the keycode followed by an "Esc."

If a keyword needs to be placed in the middle of a list, place the cursor on the line below where you would like the new keycode added and hit the "F1" key. A new line will be opened and you can type in the keycode. Follow this with a "return," which will write in the keyword. An "Esc" will write the new pair to memory.

Toxin Knowledge System Source Code

To delete keywords you must place the cursor on the line you would like to delete and hit the "F2" key. The line will be deleted, and after an "Esc," the change will be written to memory.

.F use .176 as help

BROWSE: Query-Again

If a search is uneventful, or if one would like to perform another one, this option will allow immediate access to the screen for entry of another number.

.-177

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Update-Authors/Keywords

Author and keyword data are closely associated with the citation information and the system provides an opportunity to modify those sections right after the citation update.

.-178

TKS-MAIN ABSTRACT FIND-DATA FIND-CITATION-DATA BROWSE: Delete-this entry

This question is a safe-guard against accidentally removing something that someone took the time to enter, and which you now want to remove.

Note that you will only remove one entry (the data on the screen), not all the data linked to the citation.

.1000

CITATION DATA SCREEN: J-Source - Not currently in vocabulary

This message indicates that the particular JOURNAL source code which was entered does not exist in the system library of codes and journals. Did you remember to use the "J" prefix?

If a particular journal is not included in the system journal list, it can be added by using the option "Add" in the J-List menu. J-List is accessed by using the F5 key.

.-2200

CITATION DATA SCREEN: B-Source - Not currently in vocabulary

This message indicates that the particular BOOK source code which was entered does not exist in the system library of codes and books. This is likely to be a frequent occurrence, as compared to the frequency with which it is likely to occur with journals.

A book can be added to the system data by accessing the B-List menu using the F6 key. From there one uses the "Add" option.

.V

CITATION DATA SCREEN "Source" J-LIST: Citation information already entered

When this message appears you can follow the "Find" path (accessed via selecting AbstractMgt from the TKS-MAIN menu) to see what has been entered for that citation.

Author

When a citation is new, the Author screen comes up next. Enter the last name, a space and initials (no space between initials) of the first author as requested in the note on the bottom of the screen. Hit "return" and the cursor moves to the "sequence" area where you can enter the position of the author in the sequence of names on the publication. The program will enter the numbers (hit "return") if you enter the names in the proper order. You can add up to six names to the author list.

xxxxxxx

When you are finished, hit "Esc" once again. This writes to memory the author list and the keyword screen pops up.

.G

No CITATION entered with this number

The search process has resulted in the finding that there is no citation entered with the number you used for the search. Check the number you entered, or go to "New" in the AbstractMgt menu to enter the citation.

.H

Author data already exists for this number

You cannot add an author screen if there is already author data entered for a citation. If you wish to add an author follow the "Add" or "Find" paths utilizing the "Update" function in the BROWSE menu.

TKS Screens

```

#tkscit.per
database tkstest
screen
(
CITATION DATA SCREEN
Citation No:[f000] ] File No:[f002] ]
Source:[f001 ] File Loc.:[f003 ] Entry Date:[fdte ]
Volume/Chap: [f004] Pages: [f005a]-[f005b] Year: [f006]
Title:
[f007 ]
[f008 ]
[f009 ]
[f010 ]

Journal/Book Title:
[b0 ]

Authors [a ] Keywords [k ]
PaperOver [p ] Designs [d ] Subjects [s ] ExpoRegm [e ] Signs[f ]
)
end
tables
citation

attributes
f001 = citation.citsource, reverse, autonext, upshift;
f003 = citation.citlocata, upshift, reverse, autonext, comments=
      "S = Swanson, L = Lambert, B = Beasley, P = Poison Ctr";
fdte = citation.entrydate, noupdate, reverse, default = today;
f004 = citation.citvol, reverse, autonext, zerofill, right, upshift;
f005a = citation.citpage(1,5), reverse, right, autonext, upshift;
f005b = formonly.cp2, right, reverse, autonext, upshift;
f006 = citation.citdate, reverse, autonext, upshift;
f000 = citation.citnumb, upshift, reverse, autonext;
f002 = citation.citfile, upshift, reverse, queryclear, noentry;
f007 = citation.cittitle(1,63), reverse, upshift, autonext;
f008 = formonly.ct2, reverse, upshift, autonext;
f009 = formonly.ct3, reverse, upshift, autonext;
f010 = formonly.ct4, reverse, upshift, autonext;
b0 = formonly.tmpname, noentry, noupdate;

a = formonly.authors, noentry, noupdate;
k = formonly.keywords, noentry, noupdate;
p = formonly.paperover, noentry, noupdate;
d = formonly.designs, noentry, noupdate;
s = formonly.subjects, noentry, noupdate;
e = formonly.exposures, noentry, noupdate;
f = formonly.signs, noentry, noupdate;
end

```

{

[F001

11002]

2002E]

2002]

11002]

2002]

2002

1 [£002 1

11002

1 [£002]

11f002 1

1 (£ 0 0 2)

10002 1

11002 1

1 [£002 1

11002 1

tables

attributes

```
f001 = journalst.jabrv, upshift;
```

```
f002 = journalst.jcode, upshift.
```

Instructions

```
screen record j_listing[15] (jabrv, jcode)
```

end


```
#tksaauth.per
```

```
database tkstest
```

```
screen
```

```
{
```

```
AUTHOR DATA SCREEN
```

```
Citation: [a000
```

```
] Citfile: [a001 ]
```

```
Author:
```

```
AuthSig:
```

```
[a002
```

```
]
```

```
[a003 ]
```

```
[a002
```

```
]
```

```
[a003 ]
```

```
[a002
```

```
]
```

```
[a003 ]
```

```
[a002
```

```
]
```

```
[a003 ]
```

```
}
```

```
end
```

```
tables
```

```
authors
```

```
attributes
```

```
a000 = authors.aucitnumb, reverse, upshift, autonext;
```

```
a001 = authors.aucitfile, reverse, upshift, autonext;
```

```
a002 = authors.authname, reverse, upshift, autonext, comments=
```

```
"Last Name, space, Initials; no punctuation";
```

```
a003 = authors.authsig, reverse, autonext;
```

```
instructions
```

```
screen record a_listing[4] (authname, authsig)
```

```
end
```

Toxin Knowledge System Source Code

#tkscopy.per

database tkstest

screen

{

KEYWORD DATA SCREEN

Citation: [k000

]

Citfile: [k001

]

KeyCode:

Keyword:

[k002

]

[k003

]

[k002

]

[k003

]

[k002

]

[k003

]

[k002

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[k003

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[k002

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[k003

]

[k002

]

[k003

]

[k002

]

[k003

]

[k002

]

[k003

]

}

end

tables

keywords

attributes

k000 = keywords.keycitnumb, upshift, reverse, autonext;

k001 = keywords.keycitfile, upshift, reverse, autonext;

k002 = keywords.keycode, upshift, reverse, autonext;

k003 = keywords.keyword, upshift, reverse, autonext;

instructions

screen record k_listing[10] (keycode,keyword)

end

```
#seekeys.per
database tkstest
screen
{
KEYWORD LIST
KeyCode:      Keyword:
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
[k001      ]      [k002      ]
}
end
tables
keylist

attributes
k001 = keylist.kcode,upshift,reverse,autonext;
k002 = keylist.kword,upshift,reverse,autonext;

instructions
screen record k_list[10] (kcode,kword)
end
```

Toxin Knowledge System Source Code

#tkspaper.per

database tkstest

screen

{

PAPER OVERVIEW SCREEN

Citation Num: [f000

] File No: [f001

]

[serial]

Stated Purpose: [f002

]

Implied Purpose: [f003

]

Paper class: [a][a0][class

]

Number of Study Designs in Paper: [a1]

}

end

tables

paperover

attributes

f000 = paperover.papcitnumb, reverse, upshift, autonext;

f001 = paperover.papcitfile, reverse, upshift, autonext;

serial = paperover.papserial, noentry, nouupdate;

f002 = paperover.papstatepur, reverse, upshift, autonext;

f003 = paperover.papimppur, reverse, upshift, autonext;

a = formonly.aim, upshift, reverse, autonext;

a0 = paperover.papaaim, reverse, upshift, autonext;

a1 = paperover.papnumdsqn, reverse, upshift, autonext;

class = formonly.class, upshift;

end

```

#tkdsdsgn.per
database tkstest
screen
{
  STUDY DESIGN DATA SCREEN
  Citation No:          File No:          [serial          ]
  [f000                ] [f001                ] Design No. [c ] of [d ]

  Type of Study:      [a0] [sty                ]
  In Vivo or In Vitro: [a]  [vivvit            ]

  Controls (y/n): [b]

  Comparison Info:    [f0] [comp                ]
  Comparison Methods: [f1] [i                  ]
  Control Methods:    [f2] [contr               ]
  Control Types:      [f3] [j                  ]

  How where subjects assigned to their groups? [f4] [k                ]

  Numb. of Subject Groups: [a1]
  Numb. of Exposure Regimens: [a2]
}
end

tables
stdydsgn

attributes
f000 = stdydsgn.stycitnumb, reverse, upshift, autonext;
f001 = stdydsgn.stycitfile, reverse, upshift, autonext;
serial = stdydsgn.styserial, noentry, nouupdate;
c      = stdydsgn.stydsgncur, reverse;
d      = stdydsgn.stydsgntot, reverse;
a0     = stdydsgn.stytype, reverse, upshift, autonext;
sty    = formonly.study, noentry, nouupdate, upshift;
a      = stdydsgn.styvivit, reverse, upshift, autonext;
vivvit = formonly.vivvit, noentry, nouupdate, upshift;
b      = stdydsgn.stycntl, reverse, upshift,
include = ("Y", "N"), default = "N";

f0     = stdydsgn.stycntlcmp, reverse, upshift, autonext;
comp   = formonly.cntlcmp, upshift;
f1     = stdydsgn.stycmpmeth, reverse, upshift, autonext;
i      = formonly.comp meth, upshift;
f2     = stdydsgn.stycntlmeth, reverse, upshift, autonext;
contr  = formonly.cntlmeth, noentry, nouupdate, upshift;
f3     = stdydsgn.stycntltyp, reverse, upshift, autonext;
j      = formonly.cntltyp, noentry, nouupdate, upshift, autonext;
f4     = stdydsgn.stycntlassgn, reverse, upshift, autonext;
k      = formonly.cntlassgn, noentry, nouupdate, upshift, autonext;

a1     = stdydsgn.stynumgrp, reverse, upshift, autonext;
a2     = stdydsgn.stynumexp, reverse, upshift, autonext;

instructions

```

Toxin Knowledge System Source Code

```
screen record dsgn_rec[1] (stycitnumb,  
  stycitfile,  
  styserial,  
  stydsgncur,  
  stydsgntot  
  stype,  
  styvivit,  
  stycntl,  
  stycntlcmp,  
  stycmpmeth,  
  stycntlmeth,  
  stycntltyp,  
  stycntassgn,  
  stynumgrp,  
  stynumexp);
```

```
screen record f_only1[1] (study,  
  vivvit,  
  cntlcmp,  
  compmeth,  
  cntlmeth,  
  cntltyp,  
  cntlassgn);  
end
```

```

#tksexpo.per
database tkstest
screen
{
  EXPOSURE REGIMEN DATA SCREEN
  Citation No.: [f000 ] [exserial ]

  Regimen No.: [a2] of [c ] regimens in Study design [de][g ]

  Purpose for Exposure: [f0 ][p ]

  Agent: [f001 ]

  Dose: [f002 ] [f003 ]
  Formulation: [a0] [d ]
  Route: [a1] [e ]
  Interval: [f004 ]
  Duration: [f005 ]

  Administration Method: [f006 ]
  Scheduled Evaluation Time: [f007 ]
}
end
tables exporegm

attributes
f000 = exporegm.excitnumb, reverse, upshift, autonext;
exserial = exporegm.exserial, default = 0, noentry;
a2 = exporegm.exlink, reverse, upshift, autonext;
c = formonly.tot_numexpo;
de = formonly.dsgnlabel;
g = exporegm.exdsgnnum, reverse, upshift;
f0 = exporegm.expurpose, reverse, upshift, autonext;
p = formonly.purpose, noentry, noupdate;
f001 = exporegm.exagent, reverse, upshift, autonext;
f002 = exporegm.exdose, reverse, upshift, autonext;
f003 = exporegm.exdoseunit, reverse, upshift, autonext;
a0 = exporegm.exformul, reverse, upshift, autonext;
d = formonly.formulation, noentry, noupdate;
a1 = exporegm.exroute, reverse, upshift, autonext;
e = formonly.route, noentry, noupdate;
f004 = exporegm.exinterval, reverse, upshift, autonext;
f005 = exporegm.exduration, reverse, upshift, autonext;
f006 = exporegm.exadminmeth, reverse, upshift, autonext;
f007 = exporegm.exevaltime, reverse, upshift, autonext;

instructions
screen record exp_rec[1](excitnumb,
  exserial,
  exdsgnnum,
  exlink,
  expurpose,
  exagent,
  exdose,
  exdoseunit,
  exformul,
  exroute,

```


Toxin Knowledge System Source Code

```
    exinterval,  
    exduration,  
    exadminmeth,  
    exevaltime);  
screen record frm_only[1](tot_numexpo,  
    dsgnlabel,  
    purpose,  
    formulation,  
    route);  
end
```

```

#tkssubj.per
database tkstest
screen
(
SUBJECT GROUP DATA SCREEN
Citation No. [f000 ] [sgserial ]
Group [f ] of [num] of Design [h] [g ]

Species Breed Source
[f002 ] [f003 ] [f001 ]

Number: [f004 ]
Sex: [x] [s ]

Age: [f005][a] [au ] [ar][agerange ]
Weight: [f007][f008] [wr][wtrange ]
Height: [f009][f010]

Occupation (if appropriate): [f012 ]
Health Status of Subjects: [f013 ]

Total Number of Exposures Received: [f014 ]
)
end

tables subjgrp

attributes
f000 = subjgrp.sgcitnumb, upshift, reverse, autonext;
sgserial = subjgrp.sgserial, default= 0, noentry;
f = subjgrp.sglink, upshift, reverse, autonext;
num = formonly.tot_numsubj, noentry, noupdate;
h = formonly.dsgnlabel;
g = subjgrp.sgdsgnnum, reverse;
f002 = subjgrp.sgspecies, upshift, reverse, autonext;
f003 = subjgrp.sgbreed, upshift, reverse, autonext;
f001 = subjgrp.sgsource, upshift, reverse, autonext;
f004 = subjgrp.sgnumb, upshift, reverse, autonext;
x = subjgrp.sgsex, upshift, reverse, autonext;
s = formonly.sextrans, noentry, noupdate;
f005 = subjgrp.sgage, upshift, reverse, autonext;
a = subjgrp.sgageunit, upshift, reverse, autonext,
comments = "please enter the units in reference";
au = formonly.ageunit, noentry, noupdate;
ar = subjgrp.sgagerange, upshift, reverse;
agerange = formonly.agerange, noentry, noupdate;
f007 = subjgrp.sgt, upshift, reverse, autonext;
f008 = subjgrp.sgtunit, upshift, reverse, autonext,
comments = "please enter the units in reference";
wr = subjgrp.sgwtrange, upshift, reverse;
wtrange = formonly.wtrange, noentry, noupdate;
f009 = subjgrp.sght, upshift, reverse, autonext;
f010 = subjgrp.sghtunit, upshift, reverse, autonext,
comments = "please enter the units in reference";
f012 = subjgrp.sgoccup, upshift, reverse, autonext;
f013 = subjgrp.sghlthstat, upshift, reverse, autonext;
f014 = subjgrp.sgtotexpo, upshift, reverse, autonext;

```

Toxin Knowledge System Source Code

```
instructions
screen record sgrp_rec[1](sgcitnumb,
    sgserial,
    sgdsignum,
    sglink,
    sgspecies,
    sgbreed,
    sgsource,
    sgnumb,
    sgsex,
    sgage,
    sgageunit,
    sgagerange,
    sgwt,
    sgwtunit,
    sgwtrange,
    sght,
    sghtunit,
    sgoccup,
    sghlthstat,
    sgtotexpo);
end
```

```

#tkseg1.per
database tkstest
screen
(
EXPOSURE GROUP LINK ENTRY SCREEN
Citation Num: [f000 ] [serial ]
Exposure Group:[d ][a ][e ][s1 ] ExpoGrp [n ] of [t ]
Dsgn: [s000 ] [ds ]
Subj: [s001 ] [sg ]
Expo: [s002 ] [ex ]

```

```

)
end

```

```

tables expogrp

```

```

attributes
f000 = expogrp.egcitnumb, upshift, reverse;
serial = expogrp.egserial;
d = expogrp.egdsgnlabel, reverse, upshift;
a = expogrp.egsubglabel, reverse, upshift;
e = expogrp.egexpolabel, reverse, upshift;
s1 = expogrp.eglink, upshift, reverse;
s000 = expogrp.egdsgndsc, upshift, reverse;
ds = expogrp.egdsgn;
s001 = expogrp.egsubgdsc, upshift, reverse;
sg = expogrp.egsubg;
s002 = expogrp.egexpodsc, upshift, reverse;
ex = expogrp.egexpo;
n = formonly.egnum, reverse;
t = expogrp.egtotnum, reverse;

```

```

instructions
screen record exgp_rec[1] (egcitnumb,
    egserial,
    egdsgnlabel,
    egsubglabel,
    egexpolabel,
    eglink,
    egtotnum,
    egdsgndsc,
    egdsgn,
    egsubgdsc,
    egsubg,
    egexpodsc,

```

Toxin Knowledge System Source Code

```
egexpo);

screen record exgp_rec2[1](egcitnumb,
    egserial,
    egdsgnlabel,
    egsubglabel,
    egexpolabel,
    egtctnum,
    eglink,
    egdsgndsc,
    egdsgn,
    egsubgdsc,
    egsubg,
    egexpodsc,
    egexpo);

screen record f_only[1](egnum);

screen record exgp_1[1](eglink,
    egdsgndsc,
    egsubgdsc,
    egexpodsc);
end
```

```

#tkseg2.per
database tkstest
screen
{
  TKSEXGRP DATA SCREEN
  Total ExpoGrp:[t ]      Citation Num: [f00 ]
  Exposure Group Code: [a0 ] [serial ]
  Dsgn:[f000 ]
  Subj:[f001 ]
  Expo:[f003 ]

  Exposure Group Code: [a0 ] [serial ]
  Dsgn:[f000 ]
  Subj:[f001 ]
  Expo:[f003 ]

  Exposure Group Code: [a0 ] [serial ]
  Dsgn:[f000 ]
  Subj:[f001 ]
  Expo:[f003 ]
}
end
tables expogrp

attributes
t = expogrp.egtotnum, reverse, upshift, noentry, nouupdate;
f00 = expogrp.egcitnumb, reverse, upshift;
a0 = expogrp.eglink, reverse, upshift;
serial = expogrp.egserial;
f000 = expogrp.egdsgndsc, reverse, upshift, noentry, nouupdate;
f001 = expogrp.egsubgdsc, reverse, upshift, noentry, nouupdate;
f003 = expogrp.egexpodsc, reverse, upshift, noentry, nouupdate;

instructions
screen record exgp_rec[3] (eglink,
egserial,
egdsgndsc,
egsubgdsc,
egexpodsc)
end

```

Toxin Knowledge System Source Code

#tkscf.per

database tkstest

screen

{

CLINICAL FINDING DATA SCREEN

Citation Number: [f000] [f0]

Expo Grp: [f005] [f05]

[e001]

[e002]

[e003]

Clinical Finding: Type:[m] Site [f001] Effect [f003]

[f002]

[f004]

Change Severity Units

[a][f007] [f008] [f009]

Freq Onset Duration

[f011] [f012] [f013]

}

end

tables

clinfind

attributes

f000 = clinfind.cfcitnumb, upshift, autonext, reverse;

f0 = clinfind.cfserial;

f05 = clinfind.cfeglink;

f005 = clinfind.cfeglabel, upshift, autonext, reverse,

comments = "Exposure Group that produced effect";

m = clinfind.cftype, upshift, reverse, autonext;

f001 = clinfind.cfsitecode, upshift, autonext, reverse,

comments = "Code for Anatomical site of clinical effect";

f002 = clinfind.cfsite, upshift, autonext, reverse;

f003 = clinfind.cffindcode, upshift, autonext, reverse,

comments = "Code for Clinical effect";

f004 = clinfind.cffinding, upshift, autonext, reverse;

a = clinfind.cfchange, upshift, autonext, reverse;

f007 = formonly.change, reverse;

f008 = clinfind.cfsevvalue, upshift, autonext, reverse,

comments = "Estimate of severity or lab result value";

f009 = clinfind.cfsevunits, upshift, autonext, reverse,

comments = "Units of lab result";

f011 = clinfind.cffreq, upshift, autonext, reverse,

comments = "Frequency of occurrence as Affected/Total, eg. 3/5";

f012 = clinfind.cfonset, upshift, autonext, reverse,

comments = "Time in hours between exposure and onset of signs/findings";

f013 = clinfind.cfduration, upshift, autonext, reverse,

comments = "Duration of signs/finding in hours";

e001= formonly.egdsqndsc, upshift, autonext, reverse, noentry, nouupdate;

e002= formonly.egsubgdsc, upshift, autonext, reverse, noentry, nouupdate;

e003= formonly.egexpodsc, upshift, autonext, reverse, noentry, nouupdate;

instructions

```
screen record cf_list[1](  
  cfcitnumb,  
  cfserial,  
  cfeglink,  
  cfeglabel,  
  cftype,  
  cfsitecode,  
  cfsite,  
  cffindcode,  
  cffinding,  
  cfchange,  
  cfsevvalue,  
  cfsevunits,  
  cffreq,  
  cfonset,  
  cfduration)  
end
```


Toxin Knowledge System Source Code:

#tkssite.per

database tkstest

screen

```
{
System: [a] Organ: [b ] Location: [c   ] -->> TKS Site: [f000 ]
[f001
```

```

[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
[f1      ][f004
}
```

end

tables

tkssite

attributes

a = formonly.sys, upshift, autonext;

b = formonly.org, upshift, autonext;

c = formonly.loc, upshift, autonext;

f000 = formonly.choice;

f001 = formonly.choicename, noentry, nouupdate;

f1 =formonly.holdcode;

f004 =formonly.holdname;

instructions

screen record inputer(1) (sys, org, loc, choice, choicename);

screen record holder(15) (holdcode, holdname);

end

```
#tkssynls.per
database tkstest
screen
{
Clinical Finding Synonym                                TKS FINDING SYNONYM SCREEN
[f001                                                    ]
}
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
[f1      ][f004                                           ]
}
end
tables
tkssite
attributes
f001 = formonly.finding, noentry, nouupdate,upshift;
f1   =formonly.holdcode,upshift;
f004 =formonly.holdname,upshift;

instructions
screen record holder[15] (holdcode, holdname);
end
```

Toxin Knowledge System Source Code

#tkscf1.per

database tkstest

screen

```
{
Clinical Finding:  Site/Matrix [f001      ]  Test/Lesion/Effect [f003      ]
[f002                                     ]
[f004                                     ]
}
```

end

tables

clinfind

attributes

f001 = formonly.sitecode, upshift, autonext, reverse,

comments = "Code for Anatomical site of clinical effect";

f002 = formonly.site, upshift, autonext, reverse;

f003 = formonly.findcode, upshift, autonext, reverse,

comments = "Code for Clinical effect";

f004 = formonly.finding, upshift, autonext, reverse;

end

```

#tkscf2.per
database tkstest
screen
{
  TKSCF2 DATA SCREEN
  Citation Number: [f000 ]
  Exposure Group:[f005 ]
  [e001 ]
  [e002 ]
  [e003 ]
}

Total number of signs:[nmb]

[num] Clinical Finding: Site [f001 ] Effect [f003 ]
[f002 ]
[f004 ]
Change Severity Units Freq Onset Duration
[f007 ] [f008 ] [f009 ] [f011 ] [f012 ] [f013 ]
}
end
tables
clinfind
attributes
f000 = clinfind.cfcitnumb, upshift, autonext, reverse;
f005 = clinfind.cfeglink, upshift, autonext, reverse,
comments = "Exposure Group that produced effect";
f001 = clinfind.cfsitecode, upshift, autonext, reverse,
comments = "Code for Anatomical site of clinical effect";
f002 = clinfind.cfsite, upshift, autonext, reverse;
f003 = clinfind.cffindcode, upshift, autonext, reverse,
comments = "Code for Clinical effect";
f004 = clinfind.cffinding, upshift, autonext, reverse;
f007 = clinfind.cfchange, upshift, autonext, reverse,
comments = "0= NOS, 1= NML, 2= DISORD, 3= INC, 4= DEC, 5= ABSC, 6=ABN PRES, 7=
ABN RATIO";
f008 = clinfind.cfsevvalue, upshift, autonext, reverse,
comments = "Estimate of severity or lab result value";
f009 = clinfind.cfsevunits, upshift, autonext, reverse,
comments = "Units of lab result";
f011 = clinfind.cffreq, upshift, autonext, reverse,
comments = "Frequency of occurrence as Affected/Total, eg. 3/5";
f012 = clinfind.cfonset, upshift, autonext, reverse,
comments = "Time in hours between exposure and onset of signs/findings";
f013 = clinfind.cfduration, upshift, autonext, reverse,
comments = "Duration of signs/finding in hours";

e001= formonly.egdsqndsc, reverse, noentry, nouupdate;
e002= formonly.egsubgdsc, reverse, noentry, nouupdate;
e003= formonly.egexpodsc, reverse, noentry, nouupdate;
nmb= formonly.totnumber, reverse, noentry, nouupdate;
num= formonly.curnumber, reverse, noentry, nouupdate;

instructions

screen record effect[1](cfcitnumb,
cfeglink);

```

Toxin Knowledge System Source Code

```
screen record egclinfind[1](cfsitecode,  
cfsite,  
cffindcode,  
cffinding,  
curnumber  
    cfchange,  
cfsevvalue,  
cfsevunits,  
cffreq,  
cfonset,  
cfduration);  
end
```

```

#tkscf3.per
database tkstest
screen
{
TKSCF3 DATA SCREEN
Citation Number: [f000          ]

Clinical Finding:  Site [f001    ]      Effect [f003    ]
[f002                                     ]
[f004                                     ]

Expo Grp:  [f005          ]
[e001                                     ]
[e002                                     ]
[e003                                     ]

Change      Severity  Units      Freq      Onset      Duration
[f007       ] [f008    ] [f009     ] [f011    ] [f012     ] [f013     ]

}
end
tables
clinfind
attributes
f000 = clinfind.cfcitnumb, upshift, autonext, reverse;
f001 = clinfind.cfsitecode, upshift, autonext, reverse,
comments = "Code for Anatomical site of clinical effect";
f002 = clinfind.cfsite, upshift, autonext, reverse;
f003 = clinfind.cffindcode, upshift, autonext, reverse,
comments = "Code for Clinical effect";
f004 = clinfind.cffinding, upshift, autonext, reverse;
f005 = clinfind.cfeglink, upshift, autonext, reverse,
comments = "Exposure Group that produced effect";
f007 = clinfind.cfchange, upshift, autonext, reverse,
comments = "0= NOS, 1= NML, 2= DISORD, 3= INC, 4= DEC, 5= ABSC, 6=ABN PRES, 7=
ABN RATIO";
f008 = clinfind.cfsevvalue, upshift, autonext, reverse,
comments = "Estimate of severity or lab result value";
f009 = clinfind.cfsevunits, upshift, autonext, reverse,
comments = "Units of lab result";
f011 = clinfind.cffreq, upshift, autonext, reverse,
comments = "Frequency of occurrence as Affected/Total, eg. 3/5";
f012 = clinfind.cfonset, upshift, autonext, reverse,
comments = "Time in hours between exposure and onset of signs/findings";
f013 = clinfind.cfduration, upshift, autonext, reverse,
comments = "Duration of signs/finding in hours";

e001= formonly.egdsqndsc, upshift, autonext, reverse, noentry, nouupdate;
e002= formonly.egsubgdsc, upshift, autonext, reverse, noentry, nouupdate;
e003= formonly.egexpodsc, upshift, autonext, reverse, noentry, nouupdate;

instructions

screen record cf_list[1](
cfcitnumb,
cfsitecode,
cfsite,

```

Toxin Knowledge System Source Code

```
cffindcode,  
cffinding,  
cfeglink,  
cfchange,  
cfsevvalue,  
cfsevunits,  
cffreq,  
cfonset,  
cfduration)  
erl
```

```

#vocbook.per
database tkstest
screen
{

BOOK SOURCE DATA SCREEN

Acquistion Number: [f000          ]          Book Code: [f001  ]

Book Title:
[f002                                     ]

Edition      Volume      Year
[a0]         [a1]        [f004]

Publ'sher:[f006          ] Pub. Address:[f007          ]

Editor Name:          [f008          ]

ISBN:                [f009          ]
}
end
tables
• booklst
  attributes
    f000 = booklst.hacquis,upshift, reverse, autonext;
    f001 = booklst.bcode,upshift, reverse, autonext;
    f002 = booklst.bname,upshift, reverse, autonext;
    a0 = booklst.bedno,right, zerofill, upshift, reverse, autonext;
    a1 = booklst.bvol,upshift, reverse,right, zerofill, autonext;
    f004 = booklst.bdate,upshift, reverse, autonext;
    f006 = booklst.bpub,upshift, reverse, autonext;
    f007 = booklst.bpubplace,upshift, reverse, autonext;
    f008 = booklst.beditor,upshift, reverse, autonext;
    f009 = booklst.bisbn,upshift, reverse, autonext;
  end

```


Toxin Knowledge System Source Code

#vocjourn.per

```
database tkstest
```

screen

1

JOURNAL SOURCE DATA SCREEN

Acquistion Number: [f000]

Journal Code: [f001]

Journal Name:

[f002]

[f003]

Journal Abbreviation:

[f004]

1

end

tables

journalist

attributes

f000 = formonly.jacquis, reverse, noentry, queryclear, nouupdate;

```
f001 = journalst.jcode,reverse,upshift;
```

```
f002 = journalst.jname[1,60], reverse, autonext, upshift;
```

```
f003 = formonly.jnm, reverse, autonext, upshift;
```

f004 = journalst.jabrv, reverse, autonext,upshift;

end

```
#vockeys.per
database tkstest
screen
{

KEYWORD VOCABULARY SCREEN

KeyCode:           Keyword:
[k001      ]      [k002      ]

}
end
tables
keylist

attributes
k001 = keylist.kcode,upshift,reverse, autonext;
k002 = keylist.kword, upshift,reverse,autonext;

end
```

Toxin Knowledge System Source Code

#voclab.per

database tkstest

screen

{

TKS LAB TEST VOCABULARY

CodeNum Preferred Term

[f000][f001

}

Lab Test Category: [f][g

}

Lab Test Definition:

[f003

}

SNOMED/VET

[f005][f006

}

SYNONYMS FOR TERM

[f008][f009

}

[f008][f009

}

[f008][f009

}

[f008][f009

}

[f008][f009

}

}

end

tables

lablst labsynlst

attributes

f000 = lablst.labnum;

f001 = lablst.labterm, upshift, reverse;

f = lablst.labsys-labsynlst.labsynsys, upshift, reverse;

g = lablst.labsysname, reverse;

f003 = lablst.labdef, upshift, reverse;

f005 = lablst.labsnocde;

f006 = lablst.labsnotrm, upshift, reverse;

f008 = labsynlst.labcode;

f009 = labsynlst.labsyn, reverse, upshift;

instructions

screen record holder[5] (labcode, labsyn);

end

```

#vocmorph.per
database tkstest
screen
[
  TKS MORPHOLOGY VOCABULARY
  CodeNum Preferred Term
  [f000 ][f001
]

Morphology Definition:
[f003
]

SNOMED/VET
[f005 ][f006
]

____SYNONYMS FOR TERM____
[f008 ][f009
]
[f008 ][f009
]
[f008 ][f009
]
[f008 ][f009
]
[f008 ][f009
]
]
end
tables
morphlst
morphsynlst
attributes
f000 = morphlst.morphnum;
f001 = morphlst.morphterm, upshift, reverse;
f003 = morphlst.morphdef, upshift, reverse;
f005 = morphlst.morphsnocde;
f006 = morphlst.morphsnotrm, upshift, reverse;

f008 = morphsynlst.morphcode;
f009 = morphsynlst.morphsyn, reverse, upshift;

instructions
screen record holder[5] (morphcode, morphsyn);
end

```

Toxin Knowledge System Source Code

#vocsign.per

database tkstest

screen

{

TKS SIGN/DISEASE VOCABULARY

CodeNum Preferred Term

[f000][f001

]

System Code:[f] System Name:[f002

]

Sign/Disease Definition:

[f003

]

SNOMED/VET

[f005][f006

]

SYNONYMS FOR TERM

[f008][f009

]

[f008][f009

]

[f008][f009

]

[f008][f009

]

[f008][f009

]

)

end

tables

signlst signsynlst

attributes

f000 = signlst.signnum;

f001 = signlst.sign, upshift, reverse;

f = signlst.systemcode= signsynlst.signsynsys, upshift, reverse;

f002 = signlst.systemname, upshift, reverse;

f003 = signlst.signdef, upshift, reverse;

f005 = signlst.snocode;

f006 = signlst.snoterm, upshift, reverse;

f008 = signsynlst.signcode;

f009 = signsynlst.signsyn, reverse, upshift;

instructions

screen record holder[5] (signcode, signsyn);

end

```
#vocsite.per
database tkstest
screen
{
```

```
TKS-SITE-DATA-SCREEN
Site Code:  [f000  ]
```

```
System Code: [a]
System Name: [f001          ]
```

```
Organ Code:[a0]
Organ Name:[f003          ]
```

```
Loc Code:  [a1  ]
Loc Name:  [f005          ]
```

```
SNOMED/VET Code:  [f007  ]
}
```

```
end
```

```
tables
```

```
tkssite
```

```
attributes
```

```
f000 = tkssite.sitecode, reverse, autonext, upshift;
```

```
a = tkssite.systemcode, reverse, autonext, upshift;
```

```
f001 = tkssite.systemname, reverse, autonext;
```

```
a0 = tkssite.organcode, reverse, autonext, upshift;
```

```
f003 = tkssite.organname, reverse, autonext, upshift;
```

```
a1 = tkssite.locatecode, reverse, autonext, upshift;
```

```
f005 = tkssite.locatename, reverse, autonext, upshift;
```

```
f007 = tkssite.snotopnum, reverse, autonext, upshift;
```

```
end
```

Toxin Knowledge System Source Code

#querybib.per

database tkstest

screen

{

QUERY-BY-EXAMPLE DATA SCREEN

Citation Number: [f000] File Code: [f00]

Journ/Book Code Vol Pages Year Location

[f001] [f002] [f003] [f004] [f005]

[a01]

Title of Article or Chapter: [f006]

[f007]

[f008]

[f009]

Author

[f010]

[f011]

Keyword

[f013]

[f014]

Keycode [f016][f017][f018][f019]

}

end

tables

citation authors keywords

attributes

f000 = citation.citnumb = authors.aucitnumb = keywords.keycitnumb,upshift, reverse;

f00 = citation.citfile,upshift, reverse;

f001 = citation.citsource,upshift, reverse;

f002 = citation.citvol,upshift, reverse;

f003 = citation.citpage,upshift, reverse;

f004 = citation.citdate,upshift, reverse;

f005 = citation.citlocate,upshift, reverse;

f006 = formonly.ct1,upshift, reverse;

f007 = formonly.ct2,upshift, reverse;

f008 = formonly.ct3,upshift, reverse;

f009 = formonly.ct4,upshift, reverse;

f010 = formonly.authname,upshift, reverse;

f011 = formonly.authname2,upshift, reverse;

f013 = formonly.keyword,upshift, reverse;

f014 = formonly.keyword2,upshift, reverse;

f016 = formonly.keycode,upshift, reverse;

f017 = formonly.keycode2,upshift, reverse;

f018 = formonly.keycode3,upshift, reverse;

f019 = formonly.keycode4,upshift, reverse;

a01 = formonly.citname, noentry, nouppdate, reverse;

end

```
#allcit.per
database tkstest
screen
{
```

RAW CITATION DATA SCREEN

```
citnumb      [f000                      ]
citfile      [f011                      ]
citserial    [cserial                    ]
citsource    [f001                      ]
citvol       [f002]
citpage      [f003                      ]
citdate      [f004]
cittitle     [f005                      ]
[f006                      ]
[f007                      ]
[f008                      ]
[f009                      ]
citlocate    [f010 ]
entrydate    [fdte                      ]
}
screen
{
```

RAW AUTHOR DATA SCREEN

```
aucitnumb    [f000                      ]
aucitfile    [f013                      ]
auserial     [aserial                    ]
authname     [f014                      ]
authsig      [a0]
}
screen
{
```

RAW KEYWORD DATA SCREEN

```
keycitnumb   [f000                      ]
keycitfile   [f016                      ]
keyserial    [kserial                    ]
keyword      [f017                      ]
keycode      [f018                      ]
}
end
tables
citation
authors
keywords
attributes
f000 = citation.citnumb = authors.aucitnumb= keywords.keycitnumb,upshift;
f011 = citation.citfile,upshift;
cserial = citation.citserial;
f001 = citation.citsource,upshift;
f002 = citation.citvol,upshift;
f003 = citation.citpage,upshift;
f004 = citation.citdate,upshift;
```


Toxin Knowledge System Source Code

```
f005 = citation.cittitle[1,50],upshift;  
f006 = citation.cittitle[51,100],upshift;  
f007 = citation.cittitle[101,150],upshift;  
f008 = citation.cittitle[151,200],upshift;  
f009 = citation.cittitle[201,250],upshift;  
f010 = citation.citlocate,upshift;  
fdte = citation.entrydate;
```

```
f013 = authors.aucitfile,upshift;  
aserial = authors.auserial;  
f014 = authors.authname,upshift;  
a0 = authors.authsig,upshift;
```

```
f016 = keywords.keycitfile,upshift;  
kserial = keywords.keyserial;  
f017 = keywords.keyword,upshift;  
f018 = keywords.keycode,upshift;
```

INSTRUCTIONS

```
CITATION MASTER OF AUTHORS  
authors master of keywords
```

END

```
#allpaper.per
database tkstest
screen
```

```
{
```

```
papcitnumb      [f000
papcitfile      [f101
papserial       [papserial
papstatepur     [f102
papimppur       [f103
papaim          [z0
papnumdsgn      [f104
}
```

```
screen
```

```
{
```

```
stycitnumb      [f000
stycitfile      [f001
styserial       [styserial
stydsngnur      [f002
stydsngtot      [f003
stytype         [a0]
styvivit        [a
styentl         [b]
styentlcmp      [c
stycmpmeth      [f4]
styentlmeth     [d
styentltyp      [f5]
styentassgn     [f6]
stynumgrp       [a1]
stynumexp       [a2]
}
```

```
screen
```

```
{
```

```
sgcitnumb       [sg000
sgserial        [sgserial
sgdsngnum       [styserial
sglink          [e
sgspecies       [f009
sgbreed         [f010
sgsource        [f011
sgnumb          [f012
sgsex           [f019]
sgage           [f013] sgageunit [s] sgagerange [r]
sgwt            [f015] sgwtunit  [f7]  sgwtrange  [wr]
sght            [f017] sghtunit  [f018]
sgoccup         [f020
sghlthstat      [f021
sgtotexpo       [f022
}
```

```
screen
```

```
{
```

Toxin Knowledge System Source Code

```

excitnumb      [ex000      ]
exserial       [exserial   ]
exdsgrnum      [styserial  ]
exlink         [a3        ]
expurpose       [f025 ]
exagent        [f026      ]
exdose         [f027 ]
exdoseunit     [f028 ]
exformul       [a4]
exroute        [a5]
exinterval     [f029 ]
exduration     [f030      ]
exadminmeth    [f031      ]
exevaltime     [f032      ]
)
screen
(

egcitnumb      [eg000      ]
egserial       [egserial   ]
egtotnum       [tn]
eglink         [f041      ]
egdsgn         [styserial  ]
egdsgnlabel    [dsgnlabel  ]
egdsgndsc      [f042      ]
egsubg         [sgserial   ]
egsubglabel    [subglabel  ]
egsubgdsc      [f043      ]
egexpo         [exserial   ]
egexpolabel    [expolabel  ]
egexpodsc      [f044      ]
)
screen
(
cfcitnumb      [c000      ]
cfserial       [cfserial   ]
cfegserial     [egserial   ]
cfeglabel      [c001a     ]
cfsitecode     [c002      ]
cfsite         [c003      ]
[c004          ]
cffindcode     [c005      ]
cffinding      [c006      ]
[c007          ]
cfchange       [c008      ]
cfsevvalue     [c009      ]
cfsevunits     [c010      ]
cffreq         [c011      ]
cfonset        [c012      ]
cfduration     [c013      ]
)
end

```

tables paperover stdydsgr subjgrp exporegm expogrp clinfind

attributes

```

f000 = papcitnumb=stycitnumb, reverse, upshift,queryclear;
f101 = paperover.papcitfile,reverse,upshift,queryclear;
papserial = paperover.papserial,reverse,queryclear;
f102 = paperover.papstatepur,reverse,upshift,queryclear;
f103 = paperover.papimppur,reverse,upshift,queryclear;
z0 = paperover.papaim,reverse,upshift,queryclear;
f104 = paperover.papnumdsgn,reverse,upshift,queryclear;

f001 = stycitfile, reverse, upshift,queryclear;
styserial = stdydsgr.styserial= egdsgr= sgdsgrnum= exdsgrnum,reverse,queryclear;
f002 = stdydsgrcur, reverse, upshift,queryclear;
f003 = stdydsgr.stydsgrtot, reverse, upshift,queryclear;
a0 = stdydsgr.stytype, reverse, upshift,queryclear;
a = stdydsgr.styvivit, reverse, upshift,queryclear;
b = stdydsgr.stycntl, reverse, upshift,queryclear;
c = stdydsgr.stycntlcmp, reverse, upshift,queryclear;
f4 = stdydsgr.stycmpmeth, reverse, upshift,queryclear;
d = stdydsgr.stycntlmeth, reverse, upshift,queryclear;
f5 = stdydsgr.stycntltyp, reverse, upshift,queryclear;
f6 = stdydsgr.stycntassgr, reverse, upshift,queryclear;
a1 = stdydsgr.stynumgrp, reverse, upshift,queryclear;
a2 = stdydsgr.stynumexp, reverse, upshift,queryclear;

sg000 = sgcitnumb, reverse, upshift,queryclear;
sgserial = subjgrp.sgserial=expogrp.ogsubg,reverse,queryclear;
e = subjgrp.sglink, reverse, upshift,queryclear;
f009 = subjgrp.sgspecies, reverse, upshift,queryclear;
f010 = subjgrp.sgbreed, reverse, upshift,queryclear;
f011 = subjgrp.sgsources, reverse, upshift,queryclear;
f012 = subjgrp.sgnumb, reverse, upshift,queryclear;
f019 = subjgrp.sgsex, reverse, upshift,queryclear;
f013 = subjgrp.sgage, reverse, upshift,queryclear;
s = subjgrp.sgageunit, reverse, upshift,queryclear;
r = subjgrp.sgagerange, reverse, upshift,queryclear;
f015 = subjgrp.sgmt, reverse, upshift,queryclear;
f7 = subjgrp.sgmtunit, reverse, upshift,queryclear;
wr = subjgrp.sgwtrange, reverse, upshift,queryclear;
f017 = subjgrp.sgght, reverse, upshift,queryclear;
f018 = subjgrp.sgghtunit, reverse, upshift,queryclear;
f020 = subjgrp.sgoccup, reverse, upshift,queryclear;
f021 = subjgrp.sghlthstat, reverse, upshift,queryclear;
f022 = subjgrp.sgtotexpo, reverse, upshift,queryclear;

ex000 = excitnumb, reverse, upshift,queryclear;
exserial = exporegm.exserial=expogrp.egexpo,reverse,queryclear;
a3 = exporegm.exlink, reverse, upshift,queryclear;
f025 = exporegm.expurpose, reverse, upshift,queryclear;
f026 = exporegm.exagent, reverse, upshift,queryclear;
f027 = exporegm.exdose, reverse, upshift,queryclear;
f028 = exporegm.exdoseunit, reverse, upshift,queryclear;
a4 = exporegm.exformul, reverse, upshift,queryclear;
a5 = exporegm.exroute, reverse, upshift,queryclear;
f029 = exporegm.exinterval, reverse, upshift,queryclear;
f030 = exporegm.exduration, reverse, upshift,queryclear;

```

Toxin Knowledge System Source Code

```
f031 = exporegm.exadminmeth, reverse, upshift, queryclear;
f032 = exporegm.exevaltime, reverse, upshift, queryclear;

eg000 = egcitnumb, reverse, upshift, queryclear;
egserial = expogrp.egserial=clinfind.cfeglink, reverse, queryclear;
tn      = expogrp.egtotnum, reverse, queryclear;
f041 = expogrp.eglink, reverse, upshift, queryclear;
dsgnlabel = expogrp.egdsgnlabel;
f042 = expogrp.egdsgndsc, reverse, upshift, queryclear;
subglabell = expogrp.egsubglabell;
f043 = expogrp.egsubgdsc, reverse, upshift, queryclear;
expolabell = expogrp.egexpolabell;
f044 = expogrp.egexpodsc, reverse, upshift, queryclear;

c000 = cfcitnumb, reverse, upshift, queryclear;
cfserial = clinfind.cfserial, reverse, queryclear;
c001a = clinfind.cfeglabel, reverse, upshift, queryclear;
c002 = clinfind.cfsitecode, reverse, upshift, queryclear;
c003 = clinfind.cfsite[1,35], reverse, upshift, queryclear;
c004 = clinfind.cfsite[36,70], reverse, upshift, queryclear;
c005 = clinfind.cffindcode, reverse, upshift, queryclear;
c006 = clinfind.cffinding[1,35], reverse, upshift, queryclear;
c007 = clinfind.cffinding[36,70], reverse, upshift, queryclear;
c008 = clinfind.cfchange, reverse, upshift, queryclear;
c009 = clinfind.cfsevvalue, reverse, upshift, queryclear;
c010 = clinfind.cfsevunits, reverse, upshift, queryclear;
c011 = clinfind.cffreq, reverse, upshift, queryclear;
c012 = clinfind.cfonset, reverse, upshift, queryclear;
c013 = clinfind.cfduration, reverse, upshift, queryclear;

instructions
paperover master of stdydsgr;
stdydsgr master of subjgrp;
subjgrp master of exporegm;
exporegm master of expogrp;
expogrp master of clinfind;

composites
<stdydsgr.styserial>
<subjgrp.sgdsgnnum>
<exporegm.exdsgnnum>
<expogrp.egdsgn>;
composites
<subjgrp.egserial, subjgrp.sgdsgnnum>
<expogrp.egsubg, expogrp.egdsgn>;
composites
<exporegm.exserial, exporegm.exdsgnnum>
<expogrp.egexpo, expogrp.egdsgn>;
end
```

#rawlab.per

database tkstest

screen

{

Lab-Finding Code [f000]

Synonyms

[f001

]

[f002

]

Preferred Term

[f004

]

[f005

]

Lab Test Category: [f]

Term Definition [f006

]

[f007

]

SNOMED/VET Code [f008]

[f009

]

[f010

]

}

end

tables

labsynlst lablst

attributes

f000 = labsynlst.labcode = lablst.labnum, upshift;

f001 = labsynlst.labsyn[1,60], upshift;

f002 = labsynlst.labsyn[61,100], upshift;

f004 = lablst.labterm[1,60], upshift;

f005 = lablst.labterm[61,100], upshift;

f = lablst.labsys = labsynlst.labsynsys, upshift;

f006 = lablst.labdef[1,50], upshift;

f007 = lablst.labdef[51,100], upshift;

f008 = lablst.labsnocde, upshift;

f009 = lablst.labsnotrm[1,60], upshift;

f010 = lablst.labsnotrm[61,100], upshift;

instructions

composites <lablst.labnum, lablst.labsys>

<labsynlst.labcode, labsynlst.labsynsys>;

labsynlst master of lablst;

end

Toxin Knowledge System Source Code

#rawmorph.per

database tktest

screen

{

Morphology Code [f000]

Synonyms

[f001]

[f002]

Preferred Term

[f004]

[f005]

Term Definition [f006]

[f007]

SNOMED/VET Code [f008]

[f009]

[f010]

}

end

tables

morphsynlst morphlst

attributes

f000 = morphsynlst.morphcode = morphlst.morphnum, upshift;

f001 = morphsynlst.morphsyn(1,60), upshift;

f002 = morphsynlst.morphsyn(61,100), upshift;

f004 = morphlst.morphterm(1,60), upshift;

f005 = morphlst.morphterm(61,100), upshift;

f006 = morphlst.morphdef(1,50), upshift;

f007 = morphlst.morphdef(51,100), upshift;

f008 = morphlst.morphsnocde, upshift;

f009 = morphlst.morphsnotrm(1,60), upshift;

f010 = morphlst.morphsnotrm(61,100), upshift;

instructions

morphsynlst master of morphlst;

end

```

#rawsign.per
database tktest
screen
(

Sign-Disease Code      [f000  ]

Synonyms
[f001                  ]
[f002                  ]

Preferred Term
[f004                  ]
[f005                  ]

Term Definition        [f006                  ]
[f007                  ]

System:[f][f1          ]
SNOMED/VEI Code        [f008  ]
[f009                  ]
[f010                  ]
}
end

tables
signsynlst signlst

attributes
f000 = signsynlst.signcode = signlst.signnum, upshift;
f001 = signsynlst.signsyn[1,60], upshift;
f002 = signsynlst.signsyn[61,100], upshift;

f004 = signlst.sign[1,60], upshift;
f005 = signlst.sign[61,100], upshift;
f006 = signlst.signdef[1,50], upshift;
f007 = signlst.signdef[51,100], upshift;
f    = signlst.systemcode = signsynlst.signsynsys, upshift;
f1    = signlst.systemname;
f008 = signlst.snocode, upshift;
f009 = signlst.snoterm[1,60], upshift;
f010 = signlst.snoterm[61,100], upshift;

instructions
signsynlst master of signlst;
composites <signlst.signnum, signlst.systemcode>
          <signsynlst.signcode, signsynlst.signsynsys>;
end

```


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